Adil3884 Fuman cbn
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Adil31881 Fuman pro
Adil3237 Fuman sec
Adil3851 Ostecarth
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Adfl3851 PLA2 cbnA
Adg22611 Fuman nor
Adg2611 Human cbn
Adfl3130 PLA2 cbnA
Add61377 Fuman cbn
Adb159517 Human cbn
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Adb1301 Testcster
Acc82789 Human pho
Adb1318 HpLA2-10
Add8138 HpLA2-10
Add8138 Fuman ENZ
Add8138 Fuman ENZ
Add8138 PLA2-10
Adg8113 Fuman ENZ
Adg8137 Fuman ENZ
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Adg8137 Fuman ENZ
Adg8137 Fuman Sec

Title: Perfect score:

Sequence:

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Run on:

Scoring table:

Searched:

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Phospholipase A2; PLA2; antibacterial; immunosuppressive; vulnerary; antiinflammatory; tranquilliser; antiasthmatio; antiallergic; trauma; antirheumatio; antiarthritic; septic shock; pancreatitis; addit respiratory distress syndrome; ARDS; bronchial asthma; human; allergic rhinitis; rheumatoid arthritis; ss.
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/label= Mature_PLA2
/note= "Mature_phospholipase A2"
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/product= "PLA2"
/note= "Phospholipase A2"
59. .115
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/label= Signal_peptide
116. .484
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AAL52397
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59. .487
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  Ishizaki J, Suzuki N,
  WO200121775-A1
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Aaf73130 Mouse sec
Aaf77317 Mouse sec
Aaf77374 Murine cD
Ad113850 Osteoarth
Abv22259 Human pro
Abv238096 Human pro
Abv23366 Human pro
Abv23388 Human pro
Abv23388 Human pro
Abv25535 Human pro
Abv25535 Human pro
Abv25531 Human pro
Abv26535 Human pro
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Ab169731 Prostate
Abv94158 Breast oa
Acc46906 Human pho
Adb75500 Prostate
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                 GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                            4134886 segs, 2624710521 residues
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AAA73130
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ABV23388
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ABV28096-
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Match
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WPI; 2001-290432/30

ADB75500

Score

Result No.

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JP2000166568-A
inhibitor; ss
                  Mus musculus,
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                                                                                       This invention relates to human secretory phospholipase A2 (FLA2) protein and the gene encoding it. Inhibitors of phospholipase A2 have antibacterial; immunosuppressive; antiinflammatory; tranquilliser; vulnerary; antiasthmatic; and antiathritic activity. The FLA2 protein, agene and an anti-FLA2 antibody are useful in the diagnosis of FLA2 associated diseases e.g. septic shock, adult respiratory distress syndrome, pancreatitis, trauma, bronchial asthma, allergic rhinitis and rheumatoid arthritis. The present sequence represents human cDNA encoding FLA2
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                   Human secretory phospholipase A2 and encoded gene, useful in diagnosis and screening drug candidates for treating associated diseases e.g. septic shock, adult respiratory distress syndrome and rheumatoid
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                                                                         Claim 5; Page 45-46; 50pp; Japanese.
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The present invention describes a mouse secretory type phospholipase A2 (PLA2) protein. The mouse secretory type PLA2-like protein can be used for screening in the development of inhibitors against the function of the protein. The present sequence encodes mouse secretory type PLA2
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                                                                            type phospholipase
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80.3%; Pred. No. 2.4e-73;
iive 0; Mismatches 89
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human secretory phospholipase A2 and encoded gene, useful in diagnosis of and screening drug candidates for treating associated diseases e.g. septic shock, adult respiratory distress syndrome and rheumatoid arthritis.
                                                                                                                              Phospholipase A2; PLA2; antibacterial; immunosuppressive; vulnerary; antilinflammatory; tranquilliser; antiasthmatic; antiallergic; trauma; antirheumatic; antiarthritic; septic shock; pancreatitis; mouse; adult respiratory distress syndrome; ARDS; bronchial asthma; allergic rhinitis; rheumatoid arthritis; ss.
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                                                                                                       Murine cDNA encoding phospholipase A2 (PLA2).
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P-PSDB; AAB81021.
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144 CCCCCTGCCTACCTCCCCCAGGATGAAACCTCCCATTGCCCTGGCTTGCCTTTGCCTCCT
                                                       204 GGTGCCCCTGGCTGGCGGGAACCTGGTCCAGTTTGGAGTGATGATGATGACGGG
                                                                                                      157 CAAGTCCGCCCTGCAGTACAACGACTATGGCTGTTACTGCGGCATCGGTGGCTCCCACTG
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                                                                                                                                                                                                                                                                               384 gaagcirgogcirgigaccccaagcirgoaaaagraccircrircriarcaccacaacar
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                                   GGTGGCTCTGGTCACCGGGAACCTGGTTCAGTTTGGGGGTGATGATCGAGAAGATGACAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mouse secretory type phospholipase A2 DNA sequence SEQ ID NO:1.
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Length 883;

63.4%; Score 308.6; DB 5; Length 80.3%; Pred. No. 2.4e.73; ive 0; Mismatches 89; Indels

Best Local Similarity 80.3 Matches 362, Conservative

Query Match Best Local Similarity

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DB 5; Length 320; 66; Indels

Score 190.4; DB 5 Pred. No. 1.7e-41; 0; Mismatches 205

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264 124 324 184 384 244 444

TTCGCCGCAACCTGGGCACCTACAACCGCAAATATGCCCA

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respiratory distress syndrome, pancreatitis, trauma, bronchial asthma, allergic rhinhits and rheumatoid arthritis. The present sequence represents murine cDNA encoding PidA2 (BC.3.1.1.4). The murine sequence is used in the invention for the identification and characterisation of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       125 rescences de la contración de la contración de la contraction 
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                                                                                                                                                                                                                                                                                                                                                                                                               s Aagagangagggaaaccigcccignagiacaainaciaiggccigciarigcggigcigci
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                                                                                                                                                                              Sequence 320 BP; 78 A; 91 C; 76 G; 70 T; 0 U; 5 Other;
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al Similarity 78.5%;
249; Conservative (
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                                                                                                                                                                                                                                                                         65 electrocalcideccadicedaceaaacedariedierierearecceareaciecia 124
                                                                                                                                                                                                                                                                                                                                    265 CGGGCGTCTGGAGAAGCTGGGCTGTGAGCCCAAACTGGAAAAGTATCTTTTCTCTGTCAG 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                        325 CGAACGTGGCATTTTCTGCGCCGGCAGGACCACCTGCCAGCGGCTGACCTGCGAGTGTGA 384
                                                                                                                                                         64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Phospholipase A2; PLA2; antibacterial; immunosuppressive; vulnerary; antinflammatory; tranquilliser; antiasthmatic; antiallergic; tranma; antitheumatic; antiarthitic; septic shock; pancreatitis; mouse; adult respiratory distress syndrome; ARDS; bronchial asthma; allergic rhinitis; rheumatoid arthritis; ss.
                                                                                                                                                     AAGAGANGAGGAAACCTGCCCTGNAGTACAATNACTATGGCTGCTATTGCGGTGTCGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAAGAGGCTGCCCTCTGCTTTCGCCGCAACCTGGGCACCTACAACCGCAAATATGCCCA
                                                                                                AAGATGACAGGCAAGTCCGCCCTGCAGTACAACGACTATGGCTGTTACTGCGGCATCGGT
                                                                                                                                                                                                                       GGCTCCCACTGGCCGGT-GGACCAGACTGACTGGTGCTGCCACGCCCACGACTGCTGCTA
                                           Gaps
                                           ..
                                           Indels
               Pred. No. 1.7e-41;
0; Mismatches 66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   encoding phospholipase A2 (FLA2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hanasaki K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Page 38; 50pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAF77374 standard; cDNA; 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-SEP-2000; 2000WO-JP006344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99JP-00266616
            Best Local Similarity 78.5%;
Matches 249; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  445 TTATCCCAACAAGCTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           304 CTACCCCAACAAGCTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OS 3 ISONOGI & CO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200121775-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-JUN-2001
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Determining susceptibility of an individual to joint space narrowing, osteophyte development and/or joint pain comprises identifying whether the individual has at least one polymorphism in a polymucleotide encoding
                                                                                                          therapy;
                                                                                                       ds; gene; osteopathic; antiinflammatory; antiarthritic; gene joint space narrowing; osteophyte development; joint pain; osteoarthritis; SNP; single nucleotide polymorphism.
                                                                                 Ostecarthritis-associated polymorphic nucleotide #382
                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 382; 297pp; English.
                                                                                                                                                                                                                               19-DEC-2002; 2002WO-US041225
                                                                                                                                                                                                                                                      20-DEC-2001; 2001US-0342603P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a method of determining susceptibility of an individual to joint space narrowing and/or osteophyte development and/or joint pain comprising identifying whether the individual has at least one polymorphism in a polymucleotide encoding at least one of the protein collisted in the specification. The methods, composition and agent are useful for modulating the susceptibility of an individual to joint space narrowing and/or osteophyte development and/or joint pain that is associated with a disease, preferably osteoarthritis. The cell line and in individual having susceptibility to joint space narrowing and/or an individual having susceptibility to joint space narrowing and/or osteophyte development and/or joint pain. This sequence corresponds to the solynucleotide encoding a protein listed in the specification. (Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly from WIPO at the wipo.int/pub/published_pot_sequences).
                                                                                                                                                                                                                                                                                                                                                        120724 TTTCGCCGCAACCTGGGCACCTACAACCGCAAATATGCCCCATTATCCCAACAAGCTGTGC 120783
                                                                                                                                                                                                                                                                                                           120664 GCCGGCAGGACCACCTGCCAGCGGCTGACCTGCGAGTGTGAGAAGAGGGCTGCCCTCTGC 120723
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                                                                                                                                                                                                                                                                                                                                      463
                                                                                                                                                                                                          Sequence 180550 BP; 48214 A; 39209 C; 38150 G; 49252 T; 0 U; 5725 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cancer; cytostatic; carcinogen; pharmacodyanamic marker;
marker; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
                                                                                                                                                                                                                                                                                   GCCGGCAGGACCACCTGCCAGCGGCTGACCTGCGAGTGTGACAAGAGGGCTGCCCTCTGC
                                                                                                                                                                                                                                                                                                                                   TITCGCCGCAACCTGGGCACCTACAACGCCAAATATGCCCCATTATCCCAACAAGCTGTGC
                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                    Length 180550;
                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                  29.6%; Score 144; DB 10;
100.0%; Pred. No. 4.7e-28;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                expression marker cDNA 22250.
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                                                                                                                                                                                                                                                                                                                                                                                                  120784 ACCGGGCCCACCCGCCCTGCTGA 120807
                                                                                                                                                                                                                                                                                                                                                                                     487
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP.
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2000US-0207454P.
2000US-0211314P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 144; Conservative
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pharmacogenomic
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25-MAY-2000;
09-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-JUL-2000;
13-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-SEP-2002
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                                                                                                                                                                                                                                                                                   344
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The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV0010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether a patient is afflicted with prostate cancer: (b) monitoring the progression of prostate cancer in a patient; (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate call carcinogenic potential of a compound; (g) determining whether prostate cancer has metastesized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a patient; (l) is also useful as a pharmacodyanamic or pharmacogenomic marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                75 IGCTGGTGTTCCTTTGCCTCCTGGTGGCTCTGGTCACCGGGAACCTGGTTCAGTTTGGGG 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     252 ACGACTGCTGCTACGGGCGTCTGGAGAAGCTGGGCTGTGAGCCCAAACTGGAAAGTATC 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             354 GAATGATCAAGTTGACGACAGGAAAGGAAGCCGCACTCAGTTATGGCTTCTATGGCTGCC 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          312 TTTTCTCTGTCAGCGAACGTGGCATTTTCTGCGCCGCAGGACCACCTGCCAGCGGCTGA 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  534 AGTITAGCAACTCGGGGAGCAGAATCACCTGTGCAAAACAGGACTCCTGCAGAAGTCAAC 593
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marker; gene; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        135 TGATGATCGAGAAGATGACAGGCAAG---TCCGCCCTGCAGTACAACGACTATGGCTGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     474 ATGACTGTTGCTACAAACGTCGGAGAAACGTGGATGTGGCCACCAAATTTCTGAGCTACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              594 TGTGTGAGTGTGATAAGGCTGCTGCCACCTGTTTTGCTAGAAACAAGACGACCTACAATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         372 CCTGCGAGTGTGACAAGAGGGCTGCCCTCTGCTTTCGCCGCAACCTGGGCACCTACAACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       654 AAAAGTACCAGTACTATTCCAATAAACACTGCAGAGGAGCACCCCCCCTCGTTGCTGA 709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   432 GCAAATATGCCCATTATCCCAACAAGCTGTGCACCGGGCCCACCCGCCCTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1160 BP; 319 A; 314 C; 280 G; 238 T; 0 U; 9 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 108.8; DB 5;
Pred. No. 3.1e-19;
0; Mismatches 182;
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Page 3840; 11750pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22.3%;
ilarity 55.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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Best Local Similarity
Matches 231; Conserv
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pharmacogenomic
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cancer; cytostatic; carcinogen; pharmacodyanamic marker; marker; gene; ss.

Human prostate expression marker cDNA 23357

Human; prostate pharmacogenomic

WO200160860-A2 Homo sapiens

23-AUG-2001

(MILL-) MILLENNIUM PREDICTIVE MEDICINE

16-WAR-2000; 2000US-0189862P. 25-WAY-2000; 2000US-0207454P. 09-UUN-2000; 2000US-021314P. 18-UUL-2000; 2000US-0259007P. 13-DEC-2000; 2000US-0255281P.

20-FEB-2001; 2001WO-US005171 17-FEB-2000; 2000US-0183319P. Endege WO, Monahan JE;

Schlegel R,

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Pred. No. 3.1e-19;
); Mismatches 182; Indels 3;
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The invention relates to an isolated nucleic acid molecule (I) comprising a nuclectide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether progression of prostate cancer; (b) monitoring the progression of prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate cell carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a patient; (i) is also useful as a pharmacodyanamic or pharmacogenomic marker
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Pred. No. 3.1e-19;
0; Mismatches 182; Indels 3;
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ABV23366
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654 AAAAGTACCAGTACTATTCCAATAAACACTGCAGAGGGAGCACCCCCCCTGGTTGCTGA 709 GCAAATATGCCCATTATCCCAACAAGCTGTGCACCGGGCCCACCCCGCCCTGCTGA

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ABV23388 standard; cDNA; 1160

534 AGTTTAGCAACTCGGGGAGCAGAATCACCTGTGCAAAACAGGACTCCTGCAGAAGTCAAC

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The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether a patient is afflicted with prostate cancer; (b) monitoring the efficacy of a florest cancer in a patient; (c) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a compound to inhibiting prostate cancer in a patient; (f) assessing the efficacy of inhibiting prostate cancer in a patient; (f) assessing the prostate cell carcinogenic potential of a compound; (f) assessing the prostate cancer has netastasized in a patient; (h)
assessing the aggressiveness or indolence of prostate cancer in a patient ; (I) is also useful as a pharmacodyanamic or pharmacogenomic marker
                                                                                                                                                                                                                                                                                                           Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker; pharmacogenomic marker; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
                                                        487
                                                                                      709
                                                  GCAAATATGCCCATTATCCCAACAAGTGTGCACCGGGCCCACCCCGCCCTGA
                                                                               654 AAAAGTACCAGTACTATTCCAATAAACACTGCAGAGGGGGGCACCCCTCGTTGCTGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22.3%; Score 108.8; DB 5; Length 55.5%; Pred. No. 3.1e-19; ive 0; Mismatches 182; Indels
                                                                                                                                                                                                                                                                             prostate expression marker cDNA 29235.
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                                                                                                                                                                         ВР
                                                                                                                                                                      ABV29244 standard; cDNA; 1160
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25-MAY-2000; 2000US-0207454P.
09-JUN-2000; 2000US-0211314P.
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13-DEC-2000; 2000US-0255281P.
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The invention relates to an isolated nucleic acid molecule (I) comprising a nuclectide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether a patient is afflicted with prostate cancer; (b) monitoring the efficacy of a compound to inhibit prostate cancer in a patient; (c) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (d) assessing the efficacy of a composition for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate cell carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (h)
                                                                                                                                                                                                            cancer; cytostatic; carcinogen; pharmacodyanamic marker;
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                                                                                                                                      Human prostate expression marker cDNA 23379.
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pharmacogenomic marker; gene; ss.
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2000US-0189862P.
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2000US-0211314P.
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ABV23388;
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3; Gaps

DB 5; Length 1160;

Local Similarity 55.5 es 231; Conservative

Matches

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20-FEB-2001; 2001WO-US005171.
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assessing the aggressiveness or indolence of prostate cancer in a patient; (I) is also useful as a pharmacodyanamic or pharmacogenomic marker
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                                                                                        TGCTGGTGTTCCTTTTGCCTCCTGGTCTCTCGGTCACCGGGAACCTGGTTCAGTTTGGGG
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                                                 DB 5, Length 1160;
                            Sequence 1160 BP; 319 A; 314 C; 280 G; 238 T; 0 U; 9 Other;
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                                                 Score 108.8; DB 5;
Pred. No. 3.1e-19;
0; Mismatches 182;
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                                                 22.3%;
ilarity 55.5%;
Conservative
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                                                            Similarity
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pharmacogenomic
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The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV0010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether a patient is afflicted with prostate cancer; (b) monitoring the progression of prostate cancer; (b) monitoring the progression of prostate cancer; (c) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (f) assessing the prostate cell carcinogenic potential of a compound; (g) determining whether prostate cancer has metastissized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a patient; (i) is also useful as a pharmacodyanamic or pharmacogenomic marker
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pharmacogenomic marker, gene; ss.
prostate cells and correlating with presence of prostate cancer, useful
for detecting presence of prostate cancer, stage of prostate cancer.
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Pred. No. 3.1e-19;
0; Mismatches 182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human prostate expression marker cDNA 29212.
                                                                                                                                                                                                             Claim 1; Page 5084-5084; 11750pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          standard; cDNA; 1160
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Best Local Similarity 55.5%;
Matches 231; Conservative
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                                                                                                                                                                                                                                                                                                        The invention relates to an isolated nucleic acid molecule (I) comprising a nuclectide sequence given in Tables 1-9 (ABV0010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether patient is afflicted with prostate cancer. (b) monitoring the progression of prostate cancer in a patient; (c) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate cell carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; determining whether prostate cancer has metastasized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a patient; (l) is also useful as a pharmacodyanamic or pharmacogenomic marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGCTGGTGTTCCTTTGCCTCCTGGTGGCTCTGGTCACCGGGGACCTGGTTCAGTTTGGGG 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAATGATCAAGTTGACGACAGGAAAGGAAGCCGCACTCAGTTATGGCTTCTATGGCTGC 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  473
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGATGATCGAGAAGATGACAGGCAAG---TCCGCCCTGCAGTACAACGACTATGGCTGTT 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACGACTGCTGCTACGGGCGTCTGGAGAAGCTGGGCTGTGAGCCCAAACTGGAAAAGTATC 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Angacherictracaacereregaaacerecareregeaceaecaarricereaecraca 533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTTTCTCTGTCAGCGAACGTGGCATTTTCTGCGCCGGCAGGACCACCTGCCAGCGGCTGA 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGTTTAGCAACTCGGGGAGCAGAATCACCTGTGCAAAACAGGACTCCTGCAGAAGTCAAC 593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCTGCGAGTGTGACAAGAGGGCTGCCTCTGCTTTCGCCGCAACCTGGGCACCTACAACC 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    594 TGTGTGAGTGTGATAAGGCTGCTGCTGCTTTTGCTAGAACAAGACGACCTACAATA 653
                                                                                                                                                                                                                 Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACTGTGGCGTGGCTGGCAGAGGATCCCCCAAGGATGCAACGGATCGCTGCTGTGTCACTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1160 BP; 319 A; 314 C; 280 G; 238 T; 0 U; 9 Other;
                                                                                                                     (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC
                                                                                                                                                                                                                                                                            Claim 1; Page 6228-6229; 11750pp; English.
                                                                                                                                                        Monahan
                               16-MAR-2000; 2000US-0189862P.
25-MAY-2000; 2000US-0207454P.
09-UNA-2000; 2000US-021914P.
18-UTL-2000; 2000US-0259007P.
13-DEC-2000; 2000US-0255281P.
                  2000US-0183319P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           231; Conservative
                                                                                                                                                    Endege WO,
                                                                                                                                                                                    WPI; 2001-662795/76
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Best Local Similarity
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The invention relates to a method of determining susceptibility of an individual to joint space narrowing and/or osteophyte development and/or joint pain comprising identifying whether the individual has at least one polymorphism in a polymucleotide encoding at least one of the protein listed in the specification. The methods, composition and agent are useful for modulating the susceptibility of an individual to joint space narrowing and/or osteophyte development and/or joint pain that is associated with a disease, preferably osteoarthritis. The cell line and the non-human animal are useful for screening for an agent for diagnosing to individual having susceptibility to joint space narrowing and/or osteophyte development and/or joint pain. This sequence corresponds to the polymucleotide encoding a protein listed in the specification. (Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly from WIPO at Etp.wipo.int/pub/published_pot_sequences).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Determining susceptibility of an individual to joint space narrowing, osteophyte development and/or joint pain comprises identifying whether the individual has at least one polymorphism in a polynucleotide encoding a protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       312 TITICICTGTCAGCGAACGTGGCATTITCTGCGCCGGCAGGACCACCTGCCAGCGGCTGA 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  260 AGTTTAGCAACTCGGGGAGCAGAATCACCTGTGCAAAACAGGACTCCTGCAGAAGTCAAC 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80 GAATGATCAAGTTGACGACAGGAAAGGAAGCCGCACTCAGTTATGGCTTCTACGGCTGCC 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                252 ACGACTGCTGCTACGGGCGTCTGGAGAAGCTGGGCTGTGAGGCCCAAACTGGAAAAGTATC 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               75 TGCTGGTGTTCCTTTGCCTCCTGGTGGCTCTGGTCACCGGGAACCTGGTTCAGTTTGGGG
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                                                                                                                                                          gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                  ds; gene, osteopathic, antiinflammatory, antiarthritic, ger
joint space narrowing; osteophyte development; joint pain,
osteoarthritis; SNP; single nucleotide polymorphism.
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                                                                           Osteoarthritis-associated polymorphic nucleotide #380.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22.0%; Score 107.2; DB 10; 55.3%; Pred. No. 6e-19; ive 0; Mismatches 183;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 380; 297pp; English
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(first entry)
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Best Local Similarity 55.3
Matches 230; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jones KA, Schafer A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-559141/52.
                                                                                                                                                                                                                                                                                                                                                                                        WO2003054166-A2.
                                                                                                                                                                                                                                                                                                                 Homo sapiens,
    06-MAY-2004
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ADL13848 standard; DNA; 435

ADL13848

ADL13848 ID ADL1 XX AC ADL1

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The invention relates to a method of determining susceptibility of an individual to joint space narrowing and/or osteophyte development and/or point pain comprising identifying whether the individual has at least one polymorphism in a polymucleotide encoding at least one of the protein listed in the specification. The methods, composition and agant are narrowing and/or osteophyte development and/or joint space narrowing and/or osteophyte development and/or joint pain that is associated with a disease, preferably osteoarchritis. The cell line and an individual having susceptibility to joint space narrowing and/or osteophyte development and/or joint space narrowing and/or the polymucleotide encoding a protein listed in the specification. (Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Determining susceptibility of an individual to joint space narrowing, osteophyte development and/or joint pain comprises identifying whether the individual has at least one polymorphism in a polymucleotide encoding
                                                                320 rerereacierearabacerecrecrecrererrirecracaacaacaccaccracaara 379
CCTGCGAGTGTGACAAGAGGCTGCCCTCTGCTTTCGCCGCAACCTGGGCACCTACAACC 431
                                                                                                                                                                                        GCAAATATGCCCATTATCCCAACAAGCTGTGCACCGGGCCCACCCGGCCCTGA 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ds; gene; osteopathic; antiinflammatory; antiarthritic; gene therapy; joint space narrowing; osteophyte development; joint pain; osteoarthritis; SNP; single nucleotide polymorphism.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ostecarthritis-associated polymorphic nucleotide #379.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; SEQ ID NO 379; 297pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-559141/52.
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    372
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ADD113847

ADD113847

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22.0%;

230, Conservative

Query Match Best Local Similarity Matches 230; Conservat

0; Mismatches 183; Indels

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MEDIUM TYPE: Floppy disk
COMPUTER: DEPT COMPATIBLE
COMPUTER: DEPT COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HEREWITH
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
CLASSIFICATION NUMBER:
FILING DATE:
CLASSIFICATION NUMBER:
ATCRNEY/AGRIT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELEFRENCE. (650) 845-4166
INFORMATION C CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
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| Sequence 1207, Application US/09023655
| Patent No. 6607879
| GENERAL INPORMATION:
| APPLICANT: Cocks, Benjamin G. APPLICANT: Susan G. Stuart
| APPLICANT: Susan G. Stuart
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TYPE: nucleic acid
STRANDEDNESS: single
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; IMMEDIATE SOURCE:
LIBRARY: GENBANK
; CLONE: 9190888
US-09-023-655-1207
        Query Match
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/cgn2_6/ptodata/1/ina/PCTUS_COMB.seg:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seg:*
                              GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-888-497-31
US-09-362-230-31
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US-09-489-770-2
US-09-856-486-1
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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55.3%; Pred. No. 6.8e-22; ive 0; Mismatches 183; Indels
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ZIP: 20036-5601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: BATEN: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/186,895
FILING DATE: 27-JAN-1994
FILING DATE: 27-JAN-1994
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APPLICATION NUMBER: US/08/046,383
FILING DATE: 09-APR-1993
APPLICATION NUMBER: US/07/810,414
ATTORNEY/AGENT INFORMATION:
NAME: KGAULIS, Paul N.
REGISTRATION NUMBER: 16,773
REPRESENCE/DOCKET NUMBER: PRK/3893/93802/MJW
TELEPHONE: 202-861-3000
TELEPHONE: 202-861-3000
TELEPROMINICATION FOR SEQ ID NO: 9:
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APPLICANT: Hollis, Melvyn
APPLICANT: Medham, Maurice R.C.
APPLICANT: Gooding, Clare
APPLICANT: Groweld, Franklin G.
TITLE OF INVENTION: Expression Systems
NUMBER OF SEQUENCES: 10
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Patent No. 5538885
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Best Local Similarity
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US-08-186-895-9
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APPLICANT: Weiss, Jerrold
APPLICANT: Elsbach, Peter
APPLICANT: Liang, Ning-Sheng
APPLICANT: Liang, Ning-Sheng
APPLICANT: Liang, Ning-Sheng
APPLICANT: Liang, Ning-Sheng
TITLE OF INVENTION: ANTHACTERIAL GROUP IIA PHOSPHOLIPASE A2 AND METHODS OF USE THERE
FILE BEFRENCE: 5986/LE317US/
CURRENT APPLICATION NUMBER: US/09/740,569
CURRENT FILING DATE: 2000-12-18
PRIOR PELING DATE: 1999-12-17
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin version 3.1
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LENGTH: 479 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                         Local Similaricy
hes 229; Conservative
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ORGANISM: Homo sapiens
                                                                                                         MOLECULE TYPE: CDNA FEATURE:
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, LOCATION:
US-08-186-895-9
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LENGTH: 375
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US-09-740-569-1
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Matches
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Sequence 17, Application US/09220132
Sequence 17, Application US/09220132
Sequence 17, Application US/09220132
Sequence 17, Application US/09220132
General INFORMATION:
APPLICANT: Shyjan, Andrew W.
TITLE OF INVENTION: METHODS AND COWPOSITONS FOR THE IDENTIFICATION AND ASSESSMENT
TITLE OF INVENTION: OF PROSITIE CANCE THERAPIES AND THE DIAGNOSIS OF PROSITIE CANCE
FILE REFERENCE: 07334-074001
CURRENT APPLICATION NUMBER: US/09/220,132
CURRENT FILING DATE: 1998-13-23
PRIOR FILING DATE: 1998-03-25
PRIOR FILING DATE: 1997-12-24
NUMBER OF SEQ ID NOS: 191
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17
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; Patent No. 5972677;
; GENERAL INPORMATION:
; APPLICANT: Tischfield, Jay A.
; APPLICANT: Sellhamer, Jeffrey J.
; TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
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Pred. No. 1.1e-19;
0; Mismatches 182;
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                                                                                                                                      473 ACCCCCCCCTGCTGA 487
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Best Local Similarity 54.5%;
Matches 222; Conservative
                                                                                                                                                                                                             ACCCCTCGTTGCTGA
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; ORGANISM: Homo sapiens
US-09-220-132-17
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| Patent No. 676538
| Patent No. 676538
| GENERAL INFORMATION:
| APPLICANT: Weises, Jerrold
| APPLICANT: Lisage, Nariabacherial GROUP IIA PHOSPHOLIPASE A2 AND METHODS OF USE THERE
| TITLE OF INVENTION: ANTIBACTERIAL GROUP IIA PHOSPHOLIPASE A2 AND METHODS OF USE THERE
| CURRENT APPLICATION NUMBER: US/09/740,569
| PRIOR PELING DATE: 2002-09-25
| PRIOR APPLICATION NUMBER: US/09/740,569
| PRIOR PILING DATE: 1999-12-17
| NUMBER OF SEQ ID NOS: 5
| SEQ ID NO 1
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                                                               TATGGCTTCTACGGCTGCCACTGTGGCGTGGCTGGCAGGATCCCCCAAGGATGCAACG 120
                                                                                                                                      GACTGGTGCTGCCACGCCCACGACGACTGCTACGGGCGTCTGGAGAAGCTGGGCTGTGAG 292
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TACAACGACTATGGCTGTTACTGCGGCATCGGTGGCTCCCACTGGCCGGTGGACCAGACT
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GENERAL INCRMATION:
APPLICANT: Tischfield, Jay A.
APPLICANT: Tischfield, Jay A.
APPLICANT: Tischfield, Jay A.
APPLICANT: Tischfield, Jay A.
APPLICANT: Tischfield, Jay A.
TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
TITLE OF INVENTION: Sequences Thereby, Antisense Sequences and Nucleotide
TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
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439 IGCCCATTATCCCAACAAGCTGTGCACCGGGCCCCACCCCGCCT 485
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STREET: 200 East Broward Boulevard
CITY: Fort Lauderdale
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COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/362,230
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION:
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APPLICATION NUMBER: 08/888,497
FILING DATE:
                                                                                                                                                                                                                                                                                                                                Sequence 31, Application US/09362230
Patent No. 6352849
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ATTORNEY/AGENT INFORMATION:
NAME: MALISO, PETER J. 264
REGISTRATION NUMBER: 32,264
REFERENCE/POCKET NUMBER: IN21
TELECOMMUNICATION INFORMATION:
TELEPHONE: 305-57-2498
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INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
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, LOCATION:
US-09-362-230-31
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                                                                                                                                                                                                                                                                 Schuster
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/888,497
     TITLE OF INVENTION: Sequences and Low Molecula TITLE OF INVENTION: Encoded Thereby, Antisense TITLE OF INVENTION: Sequences Having Internal MOMBER OF SEQUENCES: 44 CORRESPONDENCE ADDRESS: ADDRESSEE: Ruden, Barnett, McClosky, Smith, ADDRESSEE: Russell PA STREET: 200 East Broward Boulevard
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 305-527-2498
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CLASSIFICATION:
PRIOR PEPLICATION DATA:
APPLICATION NUMBER: US/08/651,405
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NAME: MANSO, Peter J. REGISTRATION NUMBER: 32,264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
STRANDEDNESS: single
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
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LOCATION:
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APPLICANT: Tischfield, Jay A.
APPLICANT: Tischfield, Jay A.
APPLICANT: Tischfield, Jay A.
APPLICANT: Seilhamer, Jeffrey J.
TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
NUMBER OF SEQUENCES 4.4
ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster & ADDRESSEE: Russell PA
STREET: 200 Bast Broward Boulevard
CITY: Fort Lauderdale
STREET: Port Lauderdale
CTGGGGCGGCCGAGGAACCCCCAAGGATGGCACCGATTGGTGCTGTTGGCGCATGGCATGACCA 336
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/888,497
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CLASSIFICATION:
PRICK APPLICATION:
PRICK APPLICATION DATA:
APPLICATION NUMBER: US/08/651,405
FILING DATE:
APPLICATION NUMBER: US/08/097,354
FILING DATE:
APPLICATION NUMBER: US/08/097,354
FILING DATE: 26-UL-1993
ATTOANEY, AGENT INFORMATION:
NAME: Manso, Peter J.
REGISTRATION NUMBER: 32.264
REFERENCE/DOCKET NUMBER: 1N21044.
FILECOMMUNICATION INFORMATION:
TELECHOMORICATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INFORMATION INF
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5972677
GENERAL INFORMATION:
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MEDIUM TYPE: Floppy
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TYPE: nucleic acid
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APPLICANT: Tischfield, Jay A.
APPLICANT: Seilhamer, Jeffrey J.
TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
TITLE OF INVENTION: Sequences Thereby, Antisense Sequences and Nucleotide
TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
CORRESPONDENCES: 44
CORRESPONDENCES:
                                                  CTGCTACGGCCGTCTGGAGAAGCTGGCCTGTGAAACTGGAAAAGTATCTTTTCTC 318
                                                                                                                                                                                                                                         319 TGTCAGCGAACGTGGCATTTTCTGCGCCGGCAGGACCACCTGCCAGCGGCTGACCTGCGA 378
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CONTRY: USA
ZIP: 33301
ZUP: 33301
COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/07926
FILING DATE: 15-JUL-1994
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Ruden, Barnett, McClosky,
ADDRESSEE: Russell PA
STREET: 200 East Broward Boulevard
CITY: Fort Lauderdale
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REGISTRATION NUMBER: 32,264
REFERENCE/DOCKET NUMBER: IN21044-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 305-527-2498
TELEFAX: 305-764-4996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/097,354
FILING DATE: 26-UUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Manso, Peter J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 31, Application PC/TUS9407926 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 1014 base pairs
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STRANDEDNESS: single
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Best Local Similarity
Matches 221; Conserve
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PCT-US94-07926-31
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APPLICATION NUMBER:
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Patent No. 632849

GENERAL INFORMATION:
PAPLICANT: Tischfield, Jay A.
APPLICANT: Seilhamer, Jeffrey J.
TITLE OF INVENTION: Mammallan Phospholipase A2 Nuclectide
TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
TITLE OF INVENTION: Sequences Hard Dy Molecular Weight Amino Acid Sequences
TITLE OF INVENTION: Sequences Hard Dy Molecular Meight Amino Acid Sequences
TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rusell PA
STREET: 200 Bast Broward Boulevard
CITT: Fort Lauderdale
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                                                                                                                                                                                                              Gaps
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                                                                                                                                                                    Length 1828;
                                                                                                                                                                Query Match 17.6%; Score 85.8; DB 2; Length 1. Best Local Similarity 52.9%; Pred. No. 1.8e-15; Matches 208; Conservative 0; Mismatches 182; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/362,230
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/888,497
FILING DATE:
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MEDIUM TYPE:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
      single
                                                                                     CDS
233..643
                        TOPOLOGY: linear MOLECULE TYPE: CDNA
      STRANDEDNESS:
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                                                                                   ; NAME/KEY:
; LOCATION:
US-08-888-497-29
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US-09-362-230-29
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PGT-US94-07926-29
Sequence 29, Application PC/TUS9407926
Sequence 29, Application PC/TUS9407926
Sequence 29, Application PC/TUS9407926
Sequence 29, Application Polymore and Low Molecular Weight Amino Acid Sequences TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites NUMBER OF SEQUENCES: 44
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              438
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 85.8; DB 3;
Pred. No. 1.8e-15;
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FILING DATE: 26-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: MANES, PECET J.
REGISTRATION NUMBER: 32,264
REFERENCE/DOCKET NUMBER: IN21
TELECOMMUNICATION INFORMATION:
TELEPHONE: 305-527-4498
TELEPHONE: 305-764-4996
                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 1828 base pairs
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52.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 52.9
Matches 208; Conservative
                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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FILE REFERENCE: 209308US-4346-4346-0-PCT
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                                                                                                                                                                                                        SEQ ID NO 26
LENGTH: 878
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/07926
FILING DATE: 15-JUL-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            439 IGCCCATTATCCCAACAAGCIGTGCACCGGGCC 471
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                                                                                                                                                         FILING DATE: 15-JUL-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/097,354
FILING DATE: 26-JUL-1993
ATTORNEX/AGENT INFORMATION:
NAVE: MAINSO, PETER J. 26-JUL-181
REFERENCE/DOCKET NUMBER: 32,264
REFERENCE/DOCKET NUMBER: 1021044-5
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 305-764-4996
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 1828 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 52.9%;
Matches 208; Conservative (
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TOCATION: 233..643
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PCT-US94-07926-29
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APPLICANT: ISHIZAKI, JUN
APPLICANT: SUZUKI, NORIKO.
APPLICANT: HANGAKI, KOHJI
TITLE OF INVENTION: A HUMAN SECRETORY TYPE PHOSPHOLIPASE AZ

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Sequence 21, Application US/08888497

Sequence 21, Application US/08888497

Patent No. 5972677

GENERAL INFORMATION:

APPLICANT: Schihamer, Jeffrey J.

APPLICANT: Schihamer, Jeffrey J.

TITLE OF INVENTION: Bequences and Low Molecular Weight Amino Acid Sequences TITLE OF INVENTION: Bequences and Low Molecular Weight Amino Acid Sequences TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites

NUMBER OF SEQUENCES: 44

CORRESPONDENCE ADDRESS:

ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster & ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster & ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRE
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CURRENT APPLICATION NUMBER: US/09/8E6,486
CURRENT TILING DATE: 2001-06-11
PRIOR APPLICATION NUMBER: JP10/349608
PRIOR FILING DATE: 1998-12-09
PRIOR APPLICATION NUMBER: PCT/JP99/06844
PRIOR FILING DATE: 1999-11-07
NUMBER OF SEQ ID NOS: 29
SOFTWARE: PATCHIN VERSION 3.1
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Homo sapiens
FRATURE:
NAME/KEY: CDS
LOCATION: (29)..(463)
OTHER INFORMATION:
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LOCATION: (89)..()
OTHER INFORMATION:
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Best Local Similarity
Matches 195; Conserv
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nucleic acid
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                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                              USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                33301
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                                                                                              COUNTRY:
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Patent No. 6352849

GENERAL INFORMATION: Tischfield, Jay A. APPLICANT: Tischfield, Jay A. APPLICANT: Sellhamer, Jeffrey J. TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  945 ATGACTGTTGCTACCACAAGCTTAAGGAATATGGCTGCCAGCCCATCTTGAATGCCTATC 1004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 4325;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/898,497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13.3%; Score 64.8; DB 2;
ilarity 53.5%; Pred. No. 3.8e-09;
Conservative 0; Mismatches 132;
                                                                                                                                                                                                     FILING DATE: 26-JUL-1993
ATORNEY/AGENT INFORMATION:
NAME: MAIRSO, PECET.
REGISTRATION NUMBER: 32.264
REFERENCE/DOCKET NUMBER: IN21044-5
TELECOMMUNICATION INFORMATION:
TELECHONE: 305-527-2498
TELEFAX: 305-764-4996
                                                                                                            CLASSIFICATION:
PRIOR APPLICATION NUMBER: US/08/651,405
PILING DATE:
APPLICATION NUMBER: US 08/097,354
APPLICATION NUMBER: US 08/097,354
                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 21: SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: single
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LOCATION: 722..1195
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Simi
Matches 166;
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US-08-888-497-21
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US-09-362-230-21
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945 ATGACTGITGCTACCACAGCTTAAGGAATATGGCTGCCAGCCCATCTTGAATGCCTATC 1004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----CGCCGGCAGGACCACCT 359
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ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster
ADDRESSEE: Russell PA
STREET: 200 East Broward Boulevard
                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PILING DATE: US/09/362,230
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 64.8; DB 3;
Pred. No. 3.8e-09;
0; Mismatches 132;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 08/097,354
FILING DATE: 26-UUL-1993
ATONNEY/AGENT INFORMATION:
NAME: Manso, Peter J.
REGISTRATION NUMBER: 32,264
REFERNEK/DOCKET NUMBER: IN21044-5
TELEPHONE: 305-527-2498
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PCT-USS4-07926-21
; Sequence 21, Application PC/TUS9407926
; GENERAL INFORMATION:
                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/888,497
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 305-764-4996
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 53.5%;
Matches 166; Conservative
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                                                                               Fort Lauderdale
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722..1195
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APPLICANT: Tischfield, Jay A.

APPLICANT: Seilhamer, Jeffrey J.

TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
NUMBER OF SEQUENCES: 44

CORRESPONDENCE ADDRESS:
ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster & STREET: 200 East Broward Boulevard
CITY: Fort Lauderdale
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Pred. No. 3.8e-09;
0; Mismatches 132; Indels 12; Gaps
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COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC COMPATIBLE
COMPUTER: IEM PC COMPATIBLE
COMPARE: DATEMING SYSTEM:
OFTWARE: PATEMIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/07926
FLING APPLICATION
PRIOR APPLICATION NUMBER: US 08/097,354
FILING DATE: 25-JUL-1994
ATTONERY/AGENT INPORMERTION:
ANAME: ALLOS DESCRIPTION
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REGISTRATION NUMBER: 32,264
REGISTRATION NUMBER: 1N210
TELECOMMUNICATION INFORMATION:
TELEPHONE: 305-527-2496
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 4325 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
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Best Local Similarity 53.5%;
Matches 166; Conservative (
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, LOCATION: 722..1195
PCT-US94-07926-21
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Search completed: November 13, 2004, 06:11:26 Job time : 60 secs

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| cgn2_6/ptodata/1/pubpna/US07_FUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
| cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
| cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
| cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
| cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
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| cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
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| cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
| cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3625171 seqs, 2700493622 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                          OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                           Run on:
                                                                                                                                                                                                                                                                                                                                                                                                          Title:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Sequence 3, Apply Sequence 124, App Sequence 149, App Sequence 145, App Sequence 465, App Sequence 127, Apply Sequence 75, Appl Sequence 17, Appli Sequence 1, Appli Sequence 1, Appli Sequence 597, App Description US-09-865-866-3 US-10-205-823-324 US-10-100-926A-1498 US-10-100-926A-1498 US-10-10-926A-1498 US-10-10-926A-1498 US-10-10-926A-1465 US-10-641-643-1207 US-09-925-300-70 US-09-969-708-597 US-10-255-576-1 Query Match Length DB Score 12m4496789012 Result

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Sequence 3, Appli	Sequence 17, Appl	Sequence 10988, A	Sequence 42, Appl	Sequence 10, Appl	Sequence 603, App		_	(I)	Sequence 27949, A				Sequence 24, Appl	Seguence 194, App	Sequence 22, Appl	Sequence 7, Appli	Sequence 79, Appl	Sequence 1765, Ap	Sequence 17, Appl	91 e	'n	92	92	37	53	23	23	53	23	e 53:	53	e 53
					16 US-10-296-115-603			US-10-242-5357	16 US-10-085-783A-27949	US-09-918-995-	US-09-918-995-	10 US-09-975-456B-1	LS US-10-345-680-24	LS US-10-295-027-194	LS US-10-345-680-22	16 US-10-275-998-7	16 US-10-188-832-79	IS US-10-104-047-1765	0 US-09-981-353-17	10 US-09-918-995-16879	l3 US-10-124-591-2	15 US-10-172-118-925	16 US-10-342-887-925	10 US-09-946-374-377	14 US-10-028-072-533	14 US-10-140-808-533	14 US-10-121-049-533	14 US-10-123-904-533	14 US-10-140-470-533	14 US-10-175-746-533	14 US-10-176-918-533	14 US-10-176-921-533
																															496	
20.5	20.5	20.4	18.4	17.7	17.5	17.5	17.2	16.5	16.5	16.4					14.6							12.6	12.6	12.4	12.4	12.4	12.4	12.4	12.4	12.4	12.4	12.4
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13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

Sequence 597, Application US/09969708
Fatent No. US20020102532A1
Fatent No. US20020102532A1
Fatent No. US20020102532A1
FILES PREPARATION:
FILE REFERENCE: 689290-70
FURRENT FAPLICATION WUMBER: US/09/869,708
CURRENT FILING DATE: 2001-10-03
FRIOR APPLICATION NUMBER: US/60/237,608
FRIOR APPLICATION NUMBER: US/60/237,608
FRIOR PELING DATE: 2000-10-03
FRIOR FILING DATE: 2000-10-03
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FRIOR FILING DATE: 2000-10-03 ij 75 TGCTGGTGTTCCTTTGCCTCCTGGTGGCTCTGGTCACCGGGAACCTGGTTCAGTTTGGGG 134 155 ridecadridaricaricariandescriacadesceares de arrideres arrideres 214 TGATGATCGAGAAGATGACAGGCAAG---TCCGCCCTGCAGTACAACGACTATGGCTGTT 191 Gaps . Έ Score 107.2, DB 9, Length 854; Pred. No. 2.1e-23; 0; Mismatches 183; Indels 3; Query Match 22.0%; Best Local Similarity 55.3%; Matches 230; Conservative (ORGANISM: Homosapiens US-09-969-708-597 DNA 135 원 ò

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APPLICANT: Glacu, Xumei
APPLICANT: Anderson, Dustin
APPLICANT: Anderson, Dustin
APPLICANT: Anderson, Dustin
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERAPY OF PROSTATE CANCER
TITLE OF INVENTION: THERAPY OF PROSTATE CANCER
TITLE OF INVENTION: THERAPY OF PROSTATE CANCER
TITLE OF INVENTION: WINDER: US/10/205, 823
CURRENT FILING DATE: 2002-07-25
PRIOR FILING DATE: 2001-07-25
PRIOR APPLICATION NUMBER: 60/314,356
PRIOR FILING DATE: 2001-09-25
PRIOR FILING DATE: 2001-09-25
PRIOR FILING DATE: 2001-10-12
PRIOR FILING DATE: 2001-12-12
PRIOR APPLICATION NUMBER: 60/341,746
PRIOR FILING DATE: 2001-12-12
PRIOR APPLICATION NUMBER: 60/341,746
PRIOR FILING DATE: 2001-12-12
PRIOR APPLICATION NUMBER: 60/362,158
PRIOR STUING DATE: 2003-03-05
PRIOR STUING DATE: 2003-03-05
PRIOR STUING DATE: 2003-03-05
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Gaps
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Pred. No. 2.1e-23;
0; Mismatches 183; Indels
                                                                                                                                                                                                                       ; Sequence 324, Application US/10205823; Publication No. US20030108963A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                           APPLICANT: Scilegel, Robert .
APPLICANT: Monahan, John E.
APPLICANT: Endege, Wilson O.
APPLICANT: Gannavarapu, Manjula
APPLICANT: Gorbatcheva, Bella
APPLICANT: Hoersch, Sebastian
APPLICANT: Kamatkar, Shubhangi
APPLICANT: Wonsey, Angela M.
APPLICANT: Glatt, Karen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
22.0%;
Best Local Similarity 55.3%;
Matches 230; Conservative
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US-10-205-823-324
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Sublication No. US20030045487A1

GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Jacqueline Wyatt
TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPASE A2, GROUP IIA (SYNOVIAL) EX
FILE REPERENCE: RTS-0221
CURRENT APPLICATION NUMBER: US/09/865,866
CURRENT APPLICATION NUMBER: US/09/865,866
CURRENT PAPLICATION NUMBER: US/09/865,866
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Matches 230; Conservative
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US-09-865-866-3
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ORGANISM: Homo sapiens
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APPLICANT: BIRHARDY, DANIEL
APPLICANT: NGUYSH, CATHERINE
APPLICANT: VIENG, PATRICE
APPLICANT: VIENG, PATRICE
APPLICANT: FERT, VINCENT
TITLE OF INVENITION: GENE EXPRESSION PROFILING OF PRIMARY BREAST CARCINOMAS
TITLE OF INVENITION: USING ARRAYS OF CANDIDATE GENES
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432 GCAAATATGCCCATTATCCCAACAAGCTGTGCACCGGGCCCACCCCGGCCTGCTGA 487
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                                                                                                                                                                                                                                            APPLICANT: Mannion, Jane
APPLICANT: Mannion, Jane
APPLICANT: Gaiger, Alexander
APPLICANT: Gordon, Brian
THILE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF KIDNEY CANCER
FILE REFERENCE: 210121.524
CURRENT APPLICATION NUMBER: US/10/102,524
CURRENT FILING DATE: 2002-03-19
NUMBER OF SEQ ID NOS: 1863
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1758
LENGTH: 854
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APPLICANT: BERTUCCI, FRANCIS APPLICANT: HOULGATTE, REMI
                                                                                                                                              Sequence 1758, Application US/10102524 Publication No. US20030109434A1 GENERAL INFORMATION: APPLICANT: Algate, Paul A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Homo sapiens
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APPLICANT: He, Yudong
APPLICANT: Linsley, Peter
APPLICANT: Mao, Mao.
APPLICANT: Maco, Mac
APPLICANT: Wan 't Veer, Laura
APPLICANT: Van 't Veer, Laura
APPLICANT: Van 'd Veer, Laura
APPLICANT: Van 'd Veer, Laura
APPLICANT: Senards, Rene
TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
FILE REFERENCE: 3011-17-5-99
FURRENT APPLICATION NUMBER: 60/380,770
FRIOR FILING DATE: 2002-06-14
FRIOR FILING DATE: 2002-05-14
NUMBER OF SEQ ID NOS: 2699
SEQ ID NO 665
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: phospholipase a2, group iia (platelets, ) OTHER INFORMATION: synovial fluid) (PLA2G2A) gene. US-10-007-926A-149
FILE REFERENCE: 1546-R-00
CURRENT APPLICATION NUMBER: US/10/007,926A
CURRENT FILING DATE: 2001-12-07
PRIOR APPLICATION NUMBER: 60/254,090
PRIOR PILING DATE: 2000-12-08
NUMBER OF SEQ ID NOS: 468
SOFTWARE: Patentin Ver. 2.1
SOFTWARE: Patentin Ver. 2.1
LENGTH: 854
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5. US20030224374A1
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ORGANISM: Homo sapiens
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Publication No. US2(
GENERAL INFORMATION
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135 TGATGATCGAGAAGATGACAGGCAAG---TCCGCCCTGCAGTACAACGACTATGGCTGTT 191
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                                                                                                                                                                                                                          275 ACTGTGGCGTGGCTGGCAGGATCCCCCAAGGATGCAACGGATCGCTGCTGTGTCACTC 334
                                                                                                                                                                                                                                                                           252 ACGACTGCTGCTGCGGCGTCTGGAGAAGCTGGGCTGTGAGCCCCAAACTGGAAAAGTATC 311
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432 GCAAATATGCCCATTATCCCAACAAGTGTGCACCGGGCCCACCCCGCCCTGCTGA 487
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ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windo
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/641,643
FILING DATE: 14-Augu-2003
CLASSIFICATION: «Unknown»
PRIOR APPLICATION NUMBER: «Unknown»
APPLICATION NUMBER: «Unknown»
ATTORNEY/AGENT: INFORMATION:
NAME: Zeller, Karen J.
RAGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Cocks, Benjamin G.
Susan G. Stuart
Jeffrey J. Seilhamer
TITLE OF INVENTION: CORPOSITION FOR
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Publication No. US20040077003A1
GENERAL INFORMATION:
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TELEPHONE: (650) 855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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WATION FOR SEQ ID NO: 1207:
SEQUENCE CHARACTERISTICS:
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LIBRARY: GENBANK
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APPLICANT: Roberts, Christopher J.
APPLICANT: Roberts, Christopher J.
APPLICANT: Van 't Veer, Laura Johanna
APPLICANT: Van 't Veer, Laura Johanna
APPLICANT: Van de Vijver, Marc J.
APPLICANT: Bernards, Rene
TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
FILE REFERENCE: 9301-188-999
CURRENT APPLICATION NUMBER: US/10/342,887
CURRENT APPLICATION NUMBER: 60/298,918
PRIOR APPLICATION NUMBER: 60/380,710
PRIOR PILING DATE: 2003-06-14
PRIOR APPLICATION NUMBER: 10/172,118
PRIOR APPLICATION NUMBER: 10/172,118
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                                                                                                                                 Length 854;
                                                                                                                                                                              Indels
                                                                                                                                 DB 15;
                                                                                                                               Query Match 22.0%; Score 107.2; DB 15; Best Local Similarity 55.3%; Pred. No. 2.1e-23; Matches 230; Conservative 0; Mismatches 183;
                         DATABASE ACCESSION NUMBER: NM 000300
DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 465, Application US/10342887
Publication No. US20040058340A1
GENERAL INFORMATION:
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APPLICANT: He, Yudong
APPLICANT: Linsley, Peter S.
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SEQ ID NO 465
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US-10-342-887-465
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Best Local Sim
Matches 230;
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; Redence 70, Application US/09925300
; Retent No. US20020151681A1
; GENERAL INFORMATION:
    APPLICANT: Craig Rosen,
    APPLICANT: Steve Ruben
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
    TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
    TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
    TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
    TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
    TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
    TITLE OF INVENTION NUMBER: US/09/925,300
    CURRENT FILING DATE: 2001-08-10
    PRIOR PILING DATE: 1999-03-12
    NUMBER: OF SEQ ID NOS: 1890
    SOFTWARE: Patentin Ver. 2.0
    SEQ ID NO 70
    LENGTH: 1076
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Pred. No. 2.3e-23;
0; Mismatches 183;
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OTHER INFORMATION: n equals a,t,g, or
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Best Local Similarity 55.3%;
Matches 230; Conservative
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US-10-120-75

Sequence 75, Application US/10210120

PUBLICATION OF US2030175736A1

GENERAL INFORMATION

APPLICANT: Rubin, Mark A.

APPLICANT: Rubin, Mark A.

APPLICANT: Sreekumar, Arun

TITLE OF INVENTION: Expression Profile of Prostate Cancer

FILE REPERENT APPLICATION NUMBER: US/10/210,120

CURRENT PILING DATE: 2002-08-01

PRIOR APPLICATION NUMBER: US 60/309,581

PRIOR FILING DATE: 2001-08-02

PRIOR FILING DATE: 2001-11-15

NUMBER OF SEQ ID NOS: 123

SEQ ID NO 75

LENGTH: 967
                                                                                                                                                                                                                                  Length
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Pred. No. 2.2e-23;
0; Mismatches 183; Indels
                                                                                                                                                                                                                            Score 107.2; DB 16; Length
Pred. No. 2.1e-23;
0; Mismatches 183; Indels
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SEQUENCE DESCRIPTION: SEQ ID NO: 1207
US-10-641-643-1207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 55:3%;
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US-10-210-120-75
                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 230; Conserva
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Sequence 3, Application US/10016149
Publication No. US20030100524A1
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Jacqueline Wyatt
TITLE OF INVENTION: ANTISENSE MODULATION OF PHOSPHOLIPASE A2, GROUP V (CA2+-
TITLE OF INVENTION: DEPENDENT) EXPRESSION
FILE REFERENCE: RTS-0325
CURRENT APPLICATION WUMBER: US/10/016,149
CURRENT FILING DATE: 2001-11-01
NUMBER OF SEQ ID NOS: 84
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20.8%; Score 101.4; DB 15; Length
Best Local Similarity 56.3%; Pred. No. 1.2e-21;
Matches 211; Conservative 0; Mismatches 161; Indels
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CURRENT APPLICATION NUMBER: US/10/255,576
CURRENT FILING DATE: 2002-09-25
PRIOR APPLICATION NUMBER: US/09/740,569
PRIOR PILING DATE: 2000-12-18
PRIOR PILING DATE: 1999-12-17
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin version 3.1
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
SEQ ID NO 1
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; LOCATION: (133)...(549)
US-10-016-149-3
                                                                                                                                                                                                                                       ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-255-576-1
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APPLICANT: Bisbach, Peter
APPLICANT: Bisbach, Peter
APPLICANT: Bisbach, Peter
APPLICANT: Bisbach, Peter
APPLICANT: Bisbach, Peter
TITLE OF INVENTION: ANTIBACTERIAL GROUP IIA PHOSPHOLIPASE A2 AND METHODS OF USE THERE
FILE REFERENCE: 5986/1E917USI US/09/740,569
CURRENT APPLICATION WUMBER: US/09/740,569
CURRENT APPLICATION NUMBER: US/09/740,569
PRIOR FILING DATE: 1999-12-17
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin version 3.1
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Publication No. US20030161822A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Weiss, Jerrold
APPLICANT: Elsbach, Peter
APPLICANT: Liang, Ming-Sherrord
APPLICANT: APPLICANT: APPLICANT: FIRST
FILE REFERENCE: 5986/1E917US1
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                                                                                                                                                                                                                                Sequence 1, Application US/09740569 Publication No. US20020172668A1 GENERAL INFORMATION:
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ORGANISM: Homo sapiens
                                                                                                                                                                                        RESULT 11
US-09-740-569-1
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US-09-740-569-1
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US-10-255-576-1
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372 CCTGCGAGTGTGACAAGAGGGCTGCCTCTGCTTTCGC-CGCAACCTGGGCACCTACAAC 430
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CIGCIACGGGCGICIGGAGAAGCIGGGCTGTGAGCCCCAAACIGGAAAAGIAICIITICIC 318
                                            339 CTGCTATGGGCGGCTGGAGGAGAGGCTGCAACATTCGCACACAGTCCTACAAATACAG 398
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APPLICANT: Lilie, James
APPLICANT: Lilie, James
APPLICANT: Xu, Yongyao
APPLICANT: Wangy Youzhon
APPLICANT: Wangy Youzhon
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: PREPARY OF BREAST CANCER
FILE REFERENCE: MRI-049
CURRENT APPLICATION NUMBER: US/10/198,846
CURRENT APPLICATION NUMBER: 05/20
PRIOR APPLICATION NUMBER: 60/306,220
PRIOR PILING DATE: 2001-07-18
NUMBER OF SEQ ID NOS: 14084
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10988
LENGTH: 1068
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                                                                                                                                                                                         399 ATTOGOGIGGOGIGGICACCIGCGAGCCCGGGCCCTTCTGCCAIGTGAACCTCTGTGC
                                                                                                                                  319 TGTCAGCGAACGTGGCATTTTCTGCGCCGGCAGGACCACCTGCCAGCGGCTGACCTGCGA
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                                                                                                                                                                                                                                                                                                                                                                                                                               519 CCAATACTTTCCCAACATCCTCTGCTCCTAGGCCTCCCCAGGGAGCT 565
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Pred. No. 6.5e-21;
0; Mismatches 181;
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LOCATION: 1064, 1065, 1067, 1068

CTHER INFEMATION: n = A,T,C or G

US-10-198-846-10988
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Publication No. US20030099974A1
GENERAL INFORMATION:
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Matches 232; Conservative
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US-10-198-846-10988
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Publication No. US20040110197A1
| Publication No. US20040110197A1
| Publication No. US20040110197A1
| Publication No. US20040110197A1
| Publication No. US20040110197A1
| APPLICANT: Sation, Jodi L.
| TITLE OF INVENTION: METHOD OF DETERMINING TUMOR CHARACTERISTICS BY
| TITLE OF INVENTION: LIPID-ASSOCIATED GENES
| TITLE OF INVENTION: LIPID-ASSOCIATED GENES
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| TITLE OF INVENTION: LIPID-ASSOCIATED GENES
| TITLE OF INVENTION UNMERS: US/05/647,426
| CURRENT APPLICATION NUMBER: US/05/676,052
| PRIOR FILING DATE: 2000-09-28
| NUMBER OF SEQ ID NOS: 95
| SOCTUMES: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGTCAGCGAACGTGGCATTTTTTTGCGCCGGCAGGACCACCTGCCAGCGGCTGACCTGCGA 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GIGIGACAAGAGGCCTGCCTCTGCTTTCGCCGCAACCTGGGCCACCTACAACCGCAAATA 438
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                                                                 GTTCCTGGCTTGTAGTGTGCTGCTGTGCAAGGAGGCTTGCTGGACCTAAAATCAATGAT
      GTTCCTTTGCCTCCTGGTGACCTGGTCACCGGGAACCTGGTTCAGTTTGGGGTGATGAT
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NAME/KEY: gene
LOCATION: (1)...(1016)
OTHER INFORMATION: The sequence of the cDNA coding for Phospholipase
OTHER INFORMATION: A2
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Pred. No. 4.8e-21;
0; Mismatches 182; Indels
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LENGTH: 1016
TYPE: DNA
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AY417606 465 bp DNA linear GSS 12-DEC-2003
Homo sapiens HCM6280 gene, VIRTUAL TRANSCRIPT, partial sequence,
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Clark, A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
BG927759 HNC44-1-H
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BG181316 U1-H-EU0-
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This sequence was made by sequencing genomic exons and ordering
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
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BY010605 BY010605
CF248971 esa005 e0
BR55895 BB75385
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BY014871 BY014871
BE135238 CH230-107
BB81195 BB1195
AZ661866 IMC54017
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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Perriara, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M. Inferring nonneutral evolution from human-chimp-mouse orthologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Submitted (16-NOV-2003) Celera Rockville, MD 20850, USA
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
Location/Qualifiers
                                                                                                                            GGTGGCTCCCCACTGGCGGGTGGACCAGACTGACTGGTGCTGCCACGCCCACGACGACGGCTGC
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TTCCTTTGCCTCCTGGTGGCTCTGGTCACCGGGAACCTGGTTTCAGTTTGGGGTGATGATC
                      Trecittecerecegeregerenegesecegegaaceregiteagitiegegigalgare
                                                      GAGAAGATGACAGCCAAGTCCGCCCTGCAGTACAACGACTATGGCTGTTACTGCGGCATC
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Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
Direct Submission
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/organism="Pan troglodytes"
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Mus musculus

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

I (Dases 1 to 462)

Clark, A.G.; Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,

Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,

Reriadra, S., Wango, G., Zheng, X.H., White, T.J., Sninsky, J.J.,

Adams, M.D. and Cargill, White, T.J., Sninsky, J.J.,

Inferring nonneutral evolution from human-chimp-mouse oxthologous
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Mus musculus HCM6280 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
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This sequence was made by sequencing genomic exons and ordering them based on alignment.
                                                                        84 TCCTTTGCCTCCTGGTGGCTCTGGTCACCGGGAACCTGGTTCAGTTTGGGGTGATGATCG
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Mus musculus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1 (bases 1 to 537)
Heil,O., Ebert,L., Neubert,P., Peters,M., Radelof,U., Schneider,D.
                                                                                                                                                                                                   GATGCCCCTGGCTGGCGGGAACCTGGTCCAGTTTGGAGTGATGATTGAGAGAATGACGGG 131
                                                                                                                                                                                                                                                       CAAGICCGCCCTGCAGIACAACGACIAIGGCTGTIACIGCGGCAICGGTGCCTCCCACIG 216
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Mouse Unigeneset - RZPD2

Contact: Ina Rolfs

RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
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RZPD: IMAGD998J163883.

RZPD: IMAGD998J163883.

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RZPD: IMAGD998J163883.

RZPD: IMAGD998J163883.

RZPD: SID Geneset - RZPD2 (RZPDLIB No.981)

http://www.rzpd.de/CloneCards/Cgi-
bin/Showlib.pl.cgl/response/libNo-981 Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Fax: 449 30 32639 111

www.rzpd.de
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  Length 462;
                                          Indels
cch 63.4%; Score 308.6; DB 9; al Similarity 80.3%; Pred. No. 3.4e-70; 362; Conservative 0; Mismatches 89;
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/note="organ: uterus; vector: pT7T3D-Pac (Pharmacia) with
pregnant mouse uterus; and was then primed with a Not I -
pregnant mouse uterus; and was then primed with a Not I only of the primer. Double-stranded cDNA was ligated to Eco
RI adaptors (Pharmacia), digested with Not I and cloned
into the Not I and Eco RI sites of the modified pT7T3
vector. Library is normalized. Library was constructed by
Bento Soares and M. Fatima Bonaldo. "
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Nakaido, I., Osato, N., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yaqanaka, I., Kayosawa, H., Yaqi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C., Hume, D. A., Quackenbush, J., Schriml, L. M., Kanapin, A., Matsuda, H.,
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'organism="Mus musculus
                               'mol_type="mRNA"
'db xref="taxon:10090"
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Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V., Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaaterland, T., Gariboldi, M., Gissi, C., Godik, A., Gaugh, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedierski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lenhard, B., Lyons, P.A., Maglott, D.R., Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G., Petrovsky, N., Pilai, R., Pontius, J.U., Raid, J., Ring, B.E., Kangahima, T., Red, J.C., Red, J.U., Reid, J., Ring, B.E., Ringwald, M., Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Tasdale, R.D., Tomita, M., Verardo, R., Walming, L.G., Whushaw-Boris, A., Yanagisawa, M., Yang, I., Wang, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Walli, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yang, L., Yang, L., Makanura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Itoh, M., Kagawa, I., Miyazaki, A., Bashizume, W., Imocani, K., Ishi, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
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Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rappid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
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Cells were provided by Drs. William J Pavan, Stacie Loffus, and Denise Larson (Division of Intramural Research Genetic Disease Research Branch National Human Genome Research Institute, National Institutes of Health (NIH) Building: 49, Room 4AR2 49 Convent Drive MSC '4472 Bethesda, Maryland U.S.A) whose assistance we gratefully
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Siences Center (GSCO), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P.,
Fukuda,S., Hashizume,W., Hayashida,K., Hirozane,T., Horli,F.,
Imotani,K., Ishii,Y., Itoh,M., Ragawa,I., Kawai,J., Kojima,Y.,
Kondo,S., Konno,H., Koya,S., Miyazaki,A., Murata,M.,
Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Saito,R., Sakazume,N.,
Takeda,Y., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y.
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further details.
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Fax: 81-45-503-9216
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JOURNAL

TITLE

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Location/Qualifiers

source

FEATURES

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Musuchus Buteraca; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurcgnathi; Muridae; Murinae; Mus. I (bases 1 to 726)

S NIH-MGC http://mgc.nci.nih.gov/

National Institutes of Health, Mammalian Gene Collection (MGC)

L Unpublished (1999)

L Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Michael Brownstein
CDNA Library Preparation: Michael Brownstein Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)

NNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LIML at:

http://inage.llnl.gov

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AGENCOURT_12972149 NIH_MGC_178 Mus musculus cDNA clone
IMAGE:30297098 5′, mRNA sequence.
                                                                                                              Length 728;
                                                                                                            Score 308.6; DB 6; Length Pred. No. 3.7e-70; Mismatches 89; Indels
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ug33408.yl Soares_NMPu Mus musculus cDNA clone IMAGE:1533423 5'
similar to SW:PA2I_ERIMA P24293 PHOSPHOLIPASE AZ ISOZYME PLA-1 ;,
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              /clone="IMAGE:30297098"
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/clone_lib="NIH_MGC_19"
/note="Organ: lung and heart; Vector: pDNR-LIB; Site_1:
Sfil (ggccattatggcc); Site_2: Sfil (ggcgcctcggcc); cDNA
Sfil (ggcattatggcc); site_1 and directionally cloned. 5' and
and by oligo-dT priming and directionally cloned. 5' and
3' adaptors were used in cloning as follows:
5'-AAGCAGGTATCAACGCAAGTGGCCATTACGGCGGGG-1' and
                                                                                                                                                              5'-ATTCTAGAGGCGGGGGGGCGACATG-dT(30)NN-3'. Full-length enriched library was constructed using the Clontech carator SMART kit and size-selected to contain the 0.5 kb size fraction. Library created in the laboratory of M. Brownetein (NIMH, NIH). Note: this is a NIH_MGC Library."
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0; Mismatches 77; Indels 0
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Unpublished (1997)
Contact: Robert Strausberg,
Email: cgapbs-r@mail.nih.gov
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Mus musculus (house mouse)
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al Similarity 82.1%;
354; Conservative (
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/ Gex="female"
/ dev stage="adult"
/ lab_host="blibs"
/ lab_host="blibs"
/ lab_host="blibs"
/ lab_host="blibs"
/ lone lib="Soares NMPu"
/ lote="Organ: uterus; Vector: pT7T3D-Pac (Pharmacia) with
/ note="Organ: uterus; lst strand cDNA was prepared from
a modified polylinker; lst strand cDNA was prepared from
pregnant mouse uterus, and was then primed with a Not I -
oligo(dT) primer. Double-stranded cDNA was ligated to Eco
RI adaptors (Pharmacia), digested with Not I and cloned
into the Not I and Eco RI sites of the modified pT7T3
vector. Library is normalized. Library was constructed by
Bento Soares and M. Fatima Bonaldo. "
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Rattus norvegicus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata,
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.larity 80.1%; Pred. No. 2.1e-69;
Conservative 0; Mismatches 89;
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/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:1533423"
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

(bases 1 to 436)

Kakara, T. Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T., Hayatsu, M., Hiramoto, K., Hiraoka, T., Harotani, K., Hiraoka, T., Managaki, T., Inctani, Y., Ito, M., Kawai, J., Kojima, Y., Konno, H., Kouda, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              86
                                   1 (bases 1 to 381)
Sleeman, M., Murison, J.G., Strachan, L., Kumble, K.D., Glenn, M.P.,
McGrath, A., Grierson, A., Havukkala, I., Tan, P.L.J. and Watson, J.D.
Expressed sequence tags of cDNA clones from rat dermal papilla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BB851133 RIKEN full-length enriched, melanocyte Mus musculus cDNA clone G270014819 5', mRNA sequence.
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                             Genesia Research and Development Corporation Limited P.O. Box 50, 17 Fox St, Parnell, Auckland, New Zealand Tel: 0064 9 373 5600 Fax: 0064 9 373 2189
                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:10116"
| Tissue_type="dobrissae"
| Cell_type="dermal_papilla"
| Colone_lib="Rat_Lambda_ZAP_Express_Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 260.6; DB 2;
Pred. No. 1.3e-57;
0; Mismatches 59;
                                                                                                                                                                                                                                                                                                                                                           1. .381
/organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                       Email: m.sleeman@genesis.co.nz
Seg primer: T3 forward
High quality sequence stop: 381.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="mRNA"
/strain="Dark-Agouti"
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BB851133.1 GI:17092587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tch 53.5%; al Similarity 83.4%; 296; Conservative
                                                                                                                                                         Contact: Sleeman MA
                                                                                                                                  Unpublished (2000)
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Best Local Similarity
Matches 296; Conserv
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Email: genome-reseasor riken.jp, URL.http://genome.gsc.riken.jp/
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                                                                                                                                                                                                                                                                                                                                 Contact: Yoshihide Hayashizaki
Laboratoryr for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
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/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
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347 CTTCTGTGCTAGAAACGGCTTGCCACGGCATACCTGCCAGCTGTGACAACAGACCG 406
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                                                                                                                                                                                                                                                                                                                                                            Disruption and sequence identification of 2,000 genes in mouse embryonic stem cells
Nature 392 (6676), 608-611 (1998)
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4000 Research Forest Drive, The Woodlands, TX 77381, USA
Email: materials@lexgen.com
OmniBank Sequence Tag
Class: exon-trapped.
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39.1%; Score 190.4; DB E
Best Local Similarity 78.5%; Pred. No. 3.6e-39;
Matches 249; Conservative 0; Mismatches 66
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                                                  397 CCTCTGCTTTCGCCGCAAC 415
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OmniBank
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Mus musculus (house mouse)

Mus musculus (house mouse)

Musmicalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Muscaryota; Matazoa; Chordata; Sciurognathi; Muridae; Murinae; Muscaryota; Matazoa; Chordata; Sciurognathi; Muridae; Murinae; Muscaryota; Mammalia; Eutheria; Rodentia; Sciurognathi; Murinae; Muscaryota; Bartonic, B. C. Samin, A. Ramirez-Solis; R., Richter, L.J., Finch, R.A., Friddle, C.J., Gupta, A., Hansen, G., Huyr, Huang, W., Jaing, C., Rey, B. W. Ur., Kipp, P., Kohlhauff, B., Ma, Z.-Q., Markesich, D., Payne, R., Potter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z., Sparks, M.J., Van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N., Zhu, Q., Person, C. and Sands, A.T., Vogel, P., Walke, W., Xu, N., Zhu, Q., Person, C. and Sands, A.T., Walke, W., Xu, N., Zhu, Q., Pazon, C. and Sands, A.T., Vogel, P., Malke, W., Xu, N., Zhu, Q., Pazon, C. and Sands, A.T., Vogel, P., Malke, W., Xu, N., Zhu, Q., Pazon, C. and Sands, A.T., Vogel, P., Malke, W., Xu, N., Zhu, Q., Pazon, C. and Sands, A.T., Nogel, P., Malke, W., Zu, N., Nogel, P., Malke, W., Zu, N., Nogel, P., Malke, W., Zu, N., Nogel, P., Malke, W., Zu, N., Nogel, P., Malke, W., Zu, N., Nogel, P., Malke, W., Zu, N., Nogel, P., Malke, W., Zu, N., Nogel, P., Malke, W., Zu, N., Nogel, P., Malke, W., Zu, N., Nogel, P., Malke, W., Zu, N., Nogel, P., Malke, W., Zu, N., Nogel, P., Malke, W., Zu, N., Nogel, P., Malke, W., Zu, N., Nogel, P., Malke, W., Zu, N., Nogel, P., Malke, W., Zu, N., Nogel, P., Malke, W., Zu, N., Nogel, P., Malke, W., Zu, N., Nogel, P., Malke, W., Zu, N., Nogel, P., Malke, W., Zu, N., Nogel, P., Malke, W., Zu, N., Nogel, P., Malke, W., Zu, N., Nogel, P., Malke, W., Zu, N., Nogel, P., Malke, W., Zu, N., Nogel, P., Malke, W., Zu, N., Nogel, P., Malke, W., Zu, N., Nogel, P., Malke, W., Zu, N., Nogel, P., Malke, W., Zu, N., Nogel, P., Malke, W., Zu, N., Nogel, P., Malke, W., Zu, N., Nogel, P., Malke, W., Zu, N., Nogel, P., Malke, W., Zu, N., Nogel, P., Malke, W., Zu, N., Nogel, P., Malke, W., Zu, N., Nogel,
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CG473029 309 bp DNA linear GSS 01-OCT-2003 OST327 Mus musculus 129Sv/Ev Mus musculus genomic clone OST327,
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4000 Research Forest Drive, The Woodlands, TX 77381, USA
4000 Research Forest Drive, The Woodlands, TX 77381, USA
Email: materials@lexgen.com
Gene trap sequence tag generated by 3' RACE from mouse ES cells as
described in Zambrowicz et al (Nature. 1998 Apr 9,392 (6676):608-11)
Class: Gene Trap.
Location/Qualifiers
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79.3%; Pred. No. 1.3e-38;
tive 0; Mismatches 62;
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/organism="Mus musculus"
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GSSS.
                                                                                                                         genomic survey sequence.
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Best, Local Similarity 79.3
Matches 245; Conservative
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I (bases 1 to 342)

Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kayosawa, H., Yagi, K., Tomarn, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaacerland, T., Gariboldi, M., Gissi, C., Godik, A., Gough, J., Grimmond, S., Gariboldi, M., Gissi, C., Godik, M., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kavaji, H., Marchhonni, L., McKenzie, L., Maki, H., Nagashima, T., Numata, K., Okido, T., Perted, G., Pesole, G., Petrokry, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Schunde, X., Schneider, C., Semple, C.A., Setou, M., Yang, B.L., Wanger, L., Wahlerska, Y., Taylor, M.S., Teasdale, X.D., Tomita, M., Verardo, R., Wanner, L., Wanner, L., Wahlested, C., Semple, C.A., Setou, M., Yang, I., Hayatsu, N., Hirozane-Kishikawa-Boris, A., Yanagisawa, M., Yang, I., Hayatsu, N., Hirozane-Kishikaw-Boris, A., Yanagisawa, M., Yasunishi, A., Sakai, K., Sasaki, D., Sakai, K., Sasaki, D., Sakai, K., Sasaki, D., Shibata, K., Shibata, X., Shinaya, A., Kakawa, T., Pukuda, S., Hara, A., Hashizume, M., Inotani, Shibata, K., Shinaya, A., Kakawa, T., Pukuda, S., Hara, A., Hashizume, M., Inotani, Shibata, K., Shinaya, A., Sakai, K., Sasaki, D., Sasaki, C., Sasaki, D., Sasaki, C., Sasaki, D., Sasaki, D., Sasaki, C., Sasaki, D., Sasaki, C., Sasaki, C., Sasaki, C., Sasaki, C., Sasaki, C., Sasaki, C., Sasaki, C., Sasaki, C., Sasaki, C., Sasaki, C., Sasaki, C., Sasaki, C., Sasaki, C., Sasaki, C., Sasaki, C., Sasaki, C., Sasaki, C., Sasaki, C., Sasaki, C., Sasaki, C., Sasaki, C., Sasaki, C., Sasaki, C., Sasaki, C.
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Email: genome-resigns criken.jp, URL:http://genome.gsc.riken.jp/
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,U., Konno,H.,
Miyazaki,A., Murata,M., Nakamura,M., Nomura, K., Numazaki,R.,
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Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
                                                                        BY010605 BY010605 RIKEN full-length enriched, lung RCB-0558 LLC cDNA Mus musculus cDNA clone G730021C18 5', mRNA sequence.
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Sciences Center(GSC), Yokohama Institute
He Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: ,81-45-503-9222
                                                                                                                                                                                                                                                                                                 Mus musculus (house mouse)
Mus musculus
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KEYWORDS
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CDNA"
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1 (bases 1 to 701)
Wittzell, H., Bed'Hom, B., Morin, V., Young, J.R., Whittaker, C.J., Chausse, A.M. and Zoorob, R.

A collection of chicken ESTs from activated immune cells
Unpublished (2003)
Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              137 GGTGCCCCTGGCTGGCGGGAACCTGGTTCAGTTTGGAGTGATGATGAGAAATGACGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          197 AAAGCCTGCCTGCAGTACAATGACTATGGCTGTTGCGTGTCGGTGGCTCCCCACTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                157 CAAGTCCGCCCTGCAGTACAACGACTATGGCTGTTACTGCGGGCATGGGTGGCTCCCAACG
                       prepare mouse tissues.
Please visit our web site (http://genome.gsc.riken.go.jp) for
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Fax: 33 149 58 35 00

Fax: 33 149 58 33 81

Email: acorobevif cars.fr.

Location/Qualifiers

1. 701

/organism="Gallus gallus"
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                                                                                                                                                                                                                                                                                                                                                                                  Query Match 37.0%; Score 180.2; DB 5; Length 342; Best Local Similarity 79.7%; Pred. No. 1.7e-36; Matches 212; Conservative 0; Mismatches 54; Indels 0
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Mus musculus (house mouse)

Mus musculus (house mouse)

Mus musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 544)

S Akimura,T., Arakawa,T., Carninci,P., Furuno,M., Hanagaki,T.,

Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Imotani,K.,

Ishi, Y., Ito,M., Kawai,J., Kojima,Y., Komno,H., Kouda,M.,

Matsuyma,T., Nakamura,M., Nishi,K., Nomura,K., Numasaki,R.,

Sasaki,D., Sato,K., Shibata,K., Shinaqawa,A., Shiraki,T.,

Sogabe,Y., Suzuki,H., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,

Tanaka,T., Tomaru,A., Toya,T., Watahiki,A., Yasunishi,A.,

Muramatsu,M. and Hayashizaki,Y.,
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Fel: 81-45-503-922
Fax: 81-45-503-9216
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Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length CDNA libraries for rapid discovery of new
genes. Genome Res. . 10 (10), 1617-1630 (2000)
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                                                                                  Gaps
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                                    Length 701;
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                                  Score 147.6; DB 6;
Pred. No. 7e-28;
0; Mismatches 169;
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                                      Query Match
Best Local Similarity 59.6%;
Matches 249; Conservative
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                                                                                                                                EXEMPLY integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1711 (2000)

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RIKEN integrated sequence analysis (RISA) system--384-format
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Phasianinae; Gallus.

I (bases 1 to 520)

Min, W., Lillehoj, H.S., Ashwell, C.M., Matukumalli, L.K., van Tassel, C. and Han, J.Y.

Chicken intestinal lymphocyte EST database as a resource fo analysis of mucosal immune function

Uppublished (2003)
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Animal Parasite Diseases Laboratory
Animal and Natural Resources Institute,
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clone 1GAL 19B03 5', mRNA sequence.
CD734010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
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/clone="G270037L02"
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Gallus gallus
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Bidg.1043, BARC-East, Beltsville, MD 20705, USA
Fax: 3015048771
Fax: 3015045103
Email: hlillaho@anri.barc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
0.000925 using options -trim_alt '' -trim_fasta. Vector identified
by cross match using options -minmatch 12 -minscore 18
Plate: 19 row: B column: 03
Seq primer: ATTAGGTGACACTATAG
High quality sequence stop: 520.
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/cell type="Lymphocyte"
/dev_stage="Adult"
/lab_host="ExmBH108"
/clone_lib="IGAL - Chicken Intestinal Lymphocyte"
/note="Grygan: Intestine, Vector: pCMV-SPORT6; Site_1:
Sall; Site_2: Not!; Normalized library from chicken gut
infected with coccidia duodenum and middle gut."
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Search completed: November 13, 2004, 06:10:20 Job time : 1631 secs

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Minimum DB seg length: 0 Maximum DB seg length: 200000000

Total number of hits satisfying chosen parameters:

9053458

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : GenEmbl:*
1: 9b ba:*
2: 9b_htg:*
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12: gp_ro:*
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14: gb_un:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

AF189279 Homo sapi BC069116 Homo sapi CQ727197 Sequence BC027524 Mus muscu AF166098 Mus muscu AF12304 Gene encodi BD013141 A gene en AF112984 Mus muscu BR37217 Gene encodi BD013128 A gene en BD013128 A gene en AL55823 Human DNA AL36079 Human DNA AC116054 Rattus no AC121105 Mus muscu AL84178 Mouse DNA AY656696 Homo sapi Description SUMMARIES BD013155 AF189279 BC069116 CQ727197 BC027524 AF166098 AL844178 AY656695 AY656696 E37230 BD013141 AF112984 E37217 BD013128 DB 282515 165816 186608 483 Query Match Length 239739 100.0 4476 3083 3083 4473 3083 6474 4476 1908 1908 1908 1909 4476 1909 4476 1909 4476 Score 144 1115.2 1115.2 1110.4 1108.8 Result No. υυυ

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ALIGNMENTS

BD013155 487 bp DNA linear PAT 02-AUG-2002 A gene encoding novel human secretory type phospholipase A2. BD013155 BD013155 GI:22093344 WO 0121775-A/28. Homo sapiens (human) Homo sapiens		OS Homo sapiens (human) PN W 012175-A/28 PD 29-MAR-2001 PF 18-SEP-2000 WO 2000JP006344 PR 21-SEP-1999 JP 99P 266616 PI UNI ISHIZAKI, NORIKO SUZUKI, KOJI HANASAKI PC C12N9/20, C12N15/55, C12P21/02, C12P21/08, C07K16/40 CC FH Key Location/Qualifiers FT CDS (59). (484) FT CDS (11,00)	Location/Qualifiers 1. 487 / roganism="Homo sap/mol_type="genomic"; /db_xref="taxon:960"	tch al Similarity 100.0%; Pred. No. 3.2e-112; 487; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	1 CTGCTTTCTTCTGCTGCCTTTTATGCTCCTTGTGCACCTCCCCTTCCCGGCAACCTGGGAT 60
RESULT 1 BD013155 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	REFERENCE AUTHORS TITLE JOURNAL	COMMENT	FEATURES SOURCE ORIGIN	Query Match Best Local Matches 48	oy. Op

61 GAAATCTCCCCACGTGCTGGTGTTCCTTTGCCTCCTGGTGGCTCTGGTCACCGGGAACCT 120

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

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Altschul, S.E., Zeeberg, B., Buetow, K.H., Schefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,

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Staplecron, M., Soares, W.M., B., Bonaldo, M.F., Casavant, T.L.,

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Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Feters, G.J.,

Abramson, R.D., Millahy, S.J., Bosak, S.A., McEwan, P.J.,

Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Villalon, D.K., Malak, J.A., Gunaratne, P.H., Richards, S.,

Fahey, J., Helton, E., Ketteman, M., Madan, A., Young, A.C., Shevchenko, Y.,

Boutfard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,

Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
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Homo sapiens phospholipase A2, group IIE, mRNA (cDNA clone
MAGE:7116934), partial cds.
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ive 0; Mismatches 0;
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Matches 487; Conservative
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1 (bases 1 to 487)
Suudii, M., Ishizaki, J., Yokota, Y., Higashino, K., Ono, T., Ikeda, M., Fujii, M., Kawamoto, K. and Hanasaki, K. Structures, enzymatic properties, and expression of novel human and mouse secretory phospholipase A(2)s

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Homo sapiens group IIE secretory phospholipase A2 mRNA, complete
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Suzuki, N., Ishizaki, J., Yokota, Y., Higashino, K., Cno, T.,
Kawamoto, K. and Hansaki, K.
Direct Submission
Submitted (23-SEP-1999) Shionogi Research Laboratories,
Fukushima-ku, Sagisu 5-12-4, Osaka 553-0002, Japan
Location/Qualifiers
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// Organism="Homo sapiens"
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                                                                                                                              361 CCAGCGGCTGACCTGCGAGTGTGACAAGAGGCTGCCCTCTGCTTTCGCCGCAACCTGGG 420
                                                                                                                                                           361 CCAGCGGCTGACCTGCGAGTGTGACAAGAGGCTGCCCTCTGCTTTCGCCGCAACCTGGG 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W. Mars, Kits, such as nucleic acid arrays, comprising a majority of humanexons or transcripts, for detecting expression and other uses thereof
                                                                   GGAAAAGTATCTTTTCTCTGTCAGCGAACGTGGCATTTTCTGCGCCGGCAGGACCACCCG 360
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    CTGCCACGCCCACGACTGCTGCTACGGGCGTCTGGAGAAGCTGGGCTGTGAGCCCAAACT 300
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Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                   478
                                                                                                                                                                                                                                       CACCTACAACGGCAAATATGCCCATTATGCCAACAAGAGGTGTGCACGGGGCCCACCCCG 478
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                                             GGANAAGTATCTTTTCTCTGTCAGCGAACGTGGCATTTTCTGCGCCGGCAGGACCACCTG
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Pred. No. 3.6e-97;
0; Mismatches 1;
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PE Corporation (NY) (US)
Location/Qualifiers
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RLTCECDKRAALCFRRNLGTYNRYYAHYPNXLCTGPTP"
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                                                                                                                                             Direct Submission
Submitted (16-APR-2004) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDM, sequences Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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                                                                                                                                                                                                                                                NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: rgapbs-ramail.nih.gov
Tissue Procurement: Anup Madan, University of Iowa
CDNA Library Preparation: Anup Madan, University of Iowa
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Neurogenomics Research Lab,
200 B EMRB, University of Iowa, Iowa Ctty, IA-52242
                                                                                                                                                                                                                                                                                                                                                                                 DNA Sequencing by: Neurogenomics Research Lab, 200 B EMRB, University of Iowa, Iowa City, IA-52242 anup-madan@ulowa.edu
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Pred. No. 1.5e-109;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="IMAGE:7216934"
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product="PLA2G2E protein"
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                                                                                 PUBMED
REFERENCE
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DEFINITION

RESULT 5 BC027524

ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

REFERENCE AUTHORS

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Mus musculus
Lebrarycas (hordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
1 (bases 1 to 870)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63.4%; Score 308.6; DB 10; Length 762; 80.3%; Pred. No. 3.6e-67; ive 0; Mismatches 89; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                        group IIE"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCTGTGTACTGGGCCCACCCCACCTGTGA 483
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55._.483
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Matches 362, Conservative
                                                                                                                                                                  1. .762
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AF166098
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Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.E., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N. K.,
Hopkins, R.F., Jordan, H., Moore, T., Whax, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.M. B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, K., Gibbs, R.A.,
Fahey, J.J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,
Butferfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse CDNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Andy Chan, Starah Barber, Mabel Brown-John, Yaron Butterfield, Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth Areatherstone, Malachi Griffith, Obl Griffith, Ran Guin, Nancy Liao, Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin, Teika Olson, Diana Palmquist, Anca Petrescu, Anna Liisa Prahbu, Parvaneh Saeedi, J. R Santos, Angelique Schencch, Ursula Skalska, Duane Smallus, Jeff Stott, Miranda Tsai, George Yang, Jacquie Schein, Asim Siddiqui, Rob Holt, Marco Marra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at: http://image.llnl.gov Series: RTAK Plate: 67 Row: k Column: 16 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 6755091. Location/Qualifiers
                                                                                                                                                                                  ROD 30-JUN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 762)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (08-APR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: Marcelo Bento Soares, Ph.D.
cDNA Library Preparation: M. Bento Soares, University of Iowa
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
                                                                                                                                                           DCU4/524

Mus musculus phospholipase A2, group IIE, mRNA (cDNA clone MGC41157 IMAGE:1533423), complete cds.
                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                          BC027524.1 GI:20380622
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Direct Submission
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CCCTGCTGA 429
                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus
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AUTHORS TITLE JOURNAL

REMARK COMMENT

PUBMED REFERENCE

JOURNAL

TITLE

o O

Gaps

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156 152 216 212 276

92 96

452

REFERENCE

/organism="Mus musculus" /mol_type="mRNA"

FEATURES

336

272

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JUN ISHIZAKI, NORIKO SUZUKI, KOJI HANASAKI
CIZNIS/09, CO7K16/40, CIZNS/10, CIZN9/16, CIZQI/44//(CIZNI5/09, PC
                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CIRK,10,CIRR:91), (CIRN9/16,CIRR:91),CIRNI5/00,CIRN5/00,
(CIRNI5/00,CIRR:91),(CIRN5/00,CIRR:91)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97 GGTGGCTCTGGTCACCGGGAACCTGGTTCAGTTTGGGGGTGATGGACGAAGATGACAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                264 AAAGCCTGCCTGCAGTACAATGACTATGGCTGCTATTGCGGTGTCGGTGGCTCCCACTG
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                                                                                   E97230.1 Gill8626640

DF 2000166568-A/14.

Mus musculus (house mouse)

Mus musculus (house)

Musmalia; Eutheria; Rodentia; Sciurognathi; Muridae; E Eutheria; Rodentia; Sciurognathi; Muridae; I (bases 1 to 883)

I shizaki,J.; Suzuki,N. and Hanasaki,K.

Entent: JP 2000166568-A 14 20-JUN-2000;

Musmusculus (mouse)

Patent: JP 2000166568-A 14 20-JUN-2000;

PN 9D 20-JUN-2000

PR 99-DEC-1998 JP 1998349604

PR JUN ISHIZAKI,NORIKO SUZUKI,KOJI HANASAKI
             A2
                                                                                                                                                                                                                                                                                                                                           A2
          encoding novel mouse secretory phospholipase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 308.6; DB
Pred. No. 3.6e-67
0; Mismatches 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (166)..(591)
(223)..(591)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
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Location/Qualifiers
1. .883
                                                                         GI:18626640
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al Similarity 80.3%;
362; Conservative
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Matches 363
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AUTHORS
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BD013141
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Valentin, E., Ghomashchi, F., Gelb, M.H., Lazdunski, M. and Lambeau, G. On the diversity of secreted phospholipases A(2). Cloning, tissue distribution, and functional expression of two novel mouse group II
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2 (bases 1 to 870)

2 (bases 1 to 870)

Valentin,E., Ghomashchi,F., Gelb,M.H., Lazdunski,M. and Lambeau,G.

Direct Submission

Submitted (07-JUL-1999) IPMC, CNRS, 660, route des Lucioles,

Valbonne 06560, France

Location/Qualifiers
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Bukaryota; Metazoa; Rodentia; Sciurognathi; Muridae; Murinae; Musnaalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Muss.

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I falizaki,J.; Suzuki,N. and Hanasaki,K.

A gene encoding novel human secretory type phospholipase A2

A gene encoding novel human secretory

Batent: WO 0121775-A14 29-MAR-2001;

SHIONOGI & CO LTD, JUN ISHIZAKI,NORIKO SUZUKI,KOJI HANASAKI

SHIONOGI & CO LTD, JUN ISHIZAKI,NORIKO SUZUKI,KOJI HANASAKI

PD 29-WAR-2001

PF 18-SEP-1090 WO 266616

PI JUN ISHIZAKI,NORIKO SUZUKI,KOJI HANASAKI

PC C12N9/20,C12N15/55,C12P21/02,C12P21/08,C07K16/40 CC

FH KRY

Location/Qualifiers

FT mat_peptide (223). (591).
883 bp DNA linear PAT 02-AUG-2002 A gene encoding novel human secretory type phospholipase A2. BD013141
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63.4%; Score 308.6; DB 6
Best Local Similarity 80.3%; Pred. No. 3.6e-67,
Matches 362; Conservative 0; Mismatches 89
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Mus musculus (house mouse)
Mus musculus
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AF112984 883 bp mRNA linear ROD 23-FEB-2000 Mus musculus secretory phospholipase A2 (Pla2) mRNA, complete cds. AF112984

LOCUS DEFINITION ACCESSION

RESULT 9 AF112984

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                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1 (Bases I to 883)
Sciuruki, N., Ishizaki, J., Yokota, Y., Higashino, K., Ono, T., Ikeda, M., Fujij, N., Kawamoto, K. and Hanasaki, K. and expression of novel human and mouse secretory phospholipase A(2)s
J. Biol. Chem. 275 (8), 5785-5793 (2000)
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Ishizaki,J., Suzuki,N., Higashino,K. and Hanasaki,K.
Direct Submission
Submitced (11-DEC-1998) Shionogi Research Laboratories,
Fukushima-ku, Sagisu 5-12-4, Osaka 553-0002, Japan
Location/Qualifiers
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A2

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AL358253 101824 bp DNA linear PRI 19-SEP-2002 Human DNA sequence from clone RPI1-460G22 on chromosome 1, complete sequence.
                                                                                                        Craniata, Vertebrata, Buteleostomi,
Sciurognathi, Muridae, Murinae, Mus.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 101824)
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Direct Submission
Submitted (19-SEP-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 18A, UK. E-mail enquiries:
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                                                                                                  Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoo Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; E 1 (bases 1 to 320)
E 1 shizaki,J.; Suzuki,N. and Hanasaki,K.
A gene encoding novel human secretory type phospholipase A2 batent; WO 012175-A 1 29-MAR-2001;
SHIONGGI & CO LID, JUN ISHIZAKI,NORIKO SUZUKI,KOJI HANASAKI OS Mus musculus (mouse)
PN WO 0121775-A/1
PD 29-MAR-2001
PF 18-SEP-2000 WO 2000JP006344
PR 21-SEP-1999 JP 99P 26666
PI JUN ISHIZAKI,NORIKO SUZUKI,KOJI HANASAKI PC C12N9-JO.012N15/55.C12P21/02,C12P21/08,COTK16/40 CC FH Key
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Pred. No. 2.4e-37;
0; Mismatches 66
                                                                                                                                                                                                                                                                                                                                                                                                                    1. .320
/organism="Mus musculus"
/mol_type="genomic DNA"
/do_xref="taxon:10090"
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                        BD013128.1 GI:22093317
WO 0121775-A/1.
Mus musculus (house mouse)
Mus musculus
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AL358253.16 GI:23304623
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Homo sapiens
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Best Local Similarity
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AL358253/c
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Mus musculus
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Bukaryota, Metazoa, Chordata, Sciurognathi, Muridae, Murinae, Musmalla, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus I shizaki, J., Suzuki, N. and Hanasaki, K.
Gene encoding novel mouse secretory phospholipase A2
Patent: JP 2000166568-A 1 20-JUN-2000;
SHIONOGI & CO LTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JUN ISHIZAKI,NORIKO SUZUKI,KOJI HANASAKI
CI2N15/09,CO7K16/40,CI2N5/10,C12N9/16,C12Q1/44//{C12N15/09,
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Location/Qualifiers
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                                                                                                  B37217 320 bp DNA linear P. Gene encoding novel mouse secretory phospholipase A2.
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Best Local Similarity 78.5%; Pred. No. 2.4e-37;
Matches 249; Conservative 0; Mismatches 66;
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564 GCTGTGTACTGGGCCCACCCCACCCTGCTGA 594
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/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
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JP 2000166568-A/1
20-JUN-2000
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Gaps

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COMMENT

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Direct Submission
Submitted (09-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone .
requests: clonerequest@sanger.ac.uk
On Aug 14, 2000 this sequence version replaced gi:8919533.
                                                                                                                                                                                                                                                                                                                              Assembly program: XGAP4; Version 4.5 Sequencing vector: plasmid; 108752; 100% of reads Chemistry: Dye-terminator ET-amersham; 1% of reads Chemistry: Dye-terminator Big Dye; 98% of reads Consensus quality: 145607 bases at least Q40 Consensus quality: 15362 bases at least Q20 Insert size: 155370; sum-of-contigs Q20 Insert size: 175968, 2.3% error; agarose-fp Quality coverage: 3.40x in Q20 bases; sum-of-contigs Quality coverage: 3.40x in Q20 bases; sum-of-contigs Quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             * NOTE: This is a 'working draft' sequence. It currently consists of 22 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as * rnus of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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15208: gap of 100 bp
20077: contig of 4869 bp in length
20177: gap of 100 bp
26598: contig of 6421 bp in length
2668: gap of 100 bp
31374: contig of 5176 bp in length
31974: gap of 100 bp
3580: contig of 7606 bp in length
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9 of 4977 bp in length

f 100 bp

g of 2577 bp in length
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of 2197 bp in length
100 bp
of 3370 bp in length
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of 23297 bp in length
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of 3178 bp in length
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of 2510 bp in length
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       AUTHORS
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                                                                                                                           COMMENT
                                                                                                                                                                                   During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone ame. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality.) as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em., EMBL; Sw., SWISSPROT; Tr., TREMBL; Wp., WORNPEP; Information on the WORNPEP thtp://www.sanger.ac.uk/Projects/Celegans/wormpep This sequence chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at the formation can be found at the formation can be found at the Sanger centre Chromosome 1 Mapping Group. Further Information can be found at the Sanger centre Chromosome 1 Mapping Group. Further Information can be found at the Sanger centre Chromosome 1 Mapping Group. Further Information can be found at the Sanger centre Chromosome 1 Mapping Group. Further Information can be found at the Sanger centre Chromosome 1 Mapping of Pater de Jong. For further details see
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Homo sapiens chromosome 1 clone RP11-66M4, 22 unordered pieces.
AL360079
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Sep 23, 2002 this sequence version replaced gi:22797900.
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                                                                           Center: Wellcome Trust Sanger Institute
                                                                                                                           Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
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HTG, HTGS PHASE1; HTGS_CANCELLED.
HOMO sapiens (human)
Homo sapiens
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Best Local Similarity 100.0
Matches 144; Conservative
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RESULT 13 AL360079/c DEFINITION

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ACCESSION VERSION KEYWORDS ORGANISM

REFERENCE

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Muzny, Daraie, Wetzker, M.Lee., Abramzon, S., Adams, C., Alder, J., Adams, C., Alder, J., Allen, E., Allen, E., Allen, E., Allen, E., Allen, E., Allen, E., Allen, E., Allen, E., Allen, E., Allen, E., Allen, E., Allen, E., Allen, E., Allen, E., Allen, E., Allen, E., Allen, E., Allen, E., Allen, E., Allen, E., Allen, E., Allen, E., Allen, E., Allen, E., Allen, E., Allen, E., Allen, E., Allen, E., Allen, E., Allen, E., Allen, E., Allen, E., Allen, E., Allen, E., Allen, E., Allen, E., Earlen, M., Enes, D., Cardena, V., Chare, E., Cardena, P., Carrer, C., Coyle, E., Can, C., Coyle, M., Cree, D., Denden, C., Corden, E., Cardena, C., Corden, E., Cardena, C., Corden, E., Cardena, C., Corden, E., Cardena, C., Corden, E., Cardena, C., Corden, E., Cardena, C., Corden, E., Cardena, C., Corden, E., Cardena, C., Corden, E., Cardena, C., Corden, E., Cardena, C., Corden, E., Cardena, C., Corden, E., Cardena, C., Corden, E., Cardena, C., Corden, E., Cardena, C., Corden, C., Corden, E., Cardena, C., Corden, C., Cardena, C., Corden, C., Cardena, C., Corden, C., Cardena, C., Corden, C., Cardena, C., Corden, C., Cardena, C., Cardena, C., Cardena, C., Cardena, C., Cardena, C., Cardena, C., Cardena, C., Cardena, C., Cardena, C., Cardena, C., Cardena, C., Cardena, C., Cardena, C., Cardena, C., Cardena, C., Cardena, C., Cardena, C., Cardena, C., Cardena, C., Cardena, C., Cardena, C., Cardena, C., Cardena, C., Cardena, C., Cardena, C., Cardena, C., Cardena, C., Cardena, C., Cardena, C., Cardena, C., Cardena, C., Cardena, C., Cardena, C., Cardena, C., Cardena, C., Cardena, C., Cardena, C., Cardena, C., Cardena, C., Cardena, C., Cardena, C., Cardena, C., Cardena, C., Cardena, C., Cardena, C., Cardena, C., Cardena, C., Cardena, C., Cardena, C., Cardena, C., Cardena, C., Cardena, C., Cardena, C., Cardena, C., Cardena, C., Cardena, C., Cardena, C., Cardena, C., Cardena, C., Cardena, C., Cardena, C., Cardena, C., Cardena, C., Cardena, C., Cardena, C., Cardena, C., Cardena, C., Cardena, C., Cardena, C., Cardena, C., Cardena, C., Cardena, C., C
                                                                                                                                                 AC116054 239739 bp DNA linear HTG 10-MAY-2003
Rattus norvegicus clone CH230-38C10, *** SEQUENCING IN PROGRESS
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Direct Submission
Submitted (24-MAR-2002) Human Genome Sequencing Center, Department
                                                                                                                                                                                                                                                                                                                                   Eukaryota, Merazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                                                HTG; HTGS PHASE2; HTGS DRAFT; HTGS ENRICHED.
Rattus norvegicus (Norway rat)
Rattus norvegicus
         27202 ACCGGGCCCACCCGCCCTGA 27179
                                                                                                                                                                                                                                            AC116054.8 GI:30522289
                                                                                                                                                                                                                                       VERSION
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                                                                                                  RESULT 14
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0 138979: gap of 100 bp
144504: contrig of 5525 bp in length
5 144604: gap of 100 bp
5 157470: contrig of 12866 bp in length.
Location/Qualifiers
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100te="assembly fragment:01043"
121397. 125841-
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05342. .107538
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07639. .111008
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01800. .105241
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36370. 138879
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38980. .144504
                                                                                                               1. 157470

Organism="Homo sapiens"

/mol_type="genomic DNA"

/db xref="taxon:9606"

/chromosome="1"
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Uniect Submission

Submitted (10-MXY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, IX 77030, USA

Daylor Plaza, Houston, IX 77030, USA

On May 10, 2003 this sequence version replaced gi:24942319.

The sequence in this sequence version replaced gi:24942319.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Mithin each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun
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* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 1 contigs. Gaps between the contigs

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have

* provided by the submittor.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* I 239739: contig of 239739 bp in length.
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of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 239739)
Rat Genome Sequencing Consortium.
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160857. .162689
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                   Worley, K.C.

Submitted (13-APR-2022)

Morley, K.C.

Submitted (13-APR-2022) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 282515)

Rat Genome Sequencing Consortium.

Direct Submission

AL Submitted (15-NOV-2022) Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

O Nov 15, 2002 this sequence version replaced gi:23265558.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a caffold in the Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a caffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and criented, and separated by sized gaps filled with Ns to the estimated as assembly a contigs variant a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome table.
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NOTE: This sequence may represent more than one clone.
NOTE: This is a "working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N. but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
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/note="clone boundary
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221239. .222784
/note="wgs end extension
clone_end:Sp6"
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Best Local Similarity 87.5%;
Matches 126; Conservative
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